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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. $\,$ n.a. database search, using Smith-Waterman algorithm with gap extension penalties as well as gap opening penalties

Fri Dec 25 06:17:41 1998; MasPar time 326.16 Seconds 543.181 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-951-733-19 (1-3798) from US08951733.seq 3798

Description: Perfect Score: N.A. Sequence:

TABLE default Gap open 30; Gap extend 1 Scoring table:

Dbase 0; Query 0 Nmatch STD:

Post-processing:

88822 seqs, 23323279 bases x

Searched:

Minimum Match 0% Listing first 45 summaries

n-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 9.574; Variance 5.701; scale 1.679 Statistics:

SUMMARIES

Š	Score	Match	Query Match Length DB	DB	Ð	Description	Pred. No
. [1 67	1.8	7218	-	US-08-232-	Sequence 14, Applicati	cati 1.46e-2
• •	2 49	1.3	7218	-	US-08-232-	14,	
1-1	34	6.0	215	Н	US-08-238-	5, A	7
7	32	6.0	215	٦	US-08-238-	Sequence 5, Applicatio	
٠,	5 25	0.7	99	Н	US-08-471-	Sequence 144, Applicat	7
_	5 25	0.7	98	ч	-216-10-SD	Sequence 243, Applicat	7
	7 25	0.7	69	ч	US-08-471-	Sequence 142, Applicat	7
~	3 26	0.7	74	7	PCT-US95-1	Sequence 94, Applicati	6
٠,	3 25	0.7	74	~	PCT-US95-1	Sequence 100, Applicat	icat 2.91e-01
ĭ	26	0.7	74	7	PCT-US95-1	Sequence 100, Applicat	
7	1 26	0.7	74	7	PCT-US95-1	94, A	6
H	2 25	0.7	75	~	PCT-US95-1	Sequence 99, Applicati	7
0	3 25	0.7	75	~	PCT-US95-1	-	•
ř	1 26	0.7	81	~	PCT-US95-1	Sequence 92, Applicati	cati 9.62e-02
ä	5 25	0.7	81	N	PCT-US95-1	Sequence 98, Applicati	
ĭ	26	0.7	81	~	PCT-US95-1	Sequence 98, Applicati	cati 9.62e-02
ï	7 26	0.7	81	~	PCT-US95-1	Sequence 92, Applicati	cati 9.62e-02
∺	3 26	0.7	82	~	PCT-US95-1	Sequence 97, Applicati	cati 9.62e-02
ĭ	36	7	82	c	DC#-11595-1	200000000000000000000000000000000000000	

TELEX: 899149 INFORMATION FOR SEQ ID NO: 14:

2.91e-01 2.91e-01 2.91e-01 2.91e-01 2.49e+00	8.62e-01 8.62e-01 8.62e-01 2.49e+00	8.62e-01 8.62e-01 2.49e+00 2.49e+00	2.49e+00 2.49e+00 2.49e+00 2.49e+00	8.62e-01 2.49e+00 2.49e+00 2.49e+00	2.49e+00 8.62e-01 2.49e+00 2.49e+00
Sequence 1, Application Sequence 7, Application Sequence 2, Application Sequence 3, Application Sequence 145, Application	145, 93, A 144, 143,	143, 142, 25, A	23, 120, 2, A 18,	1, A 2, 54 11, 11,	۲ , ۲. ۲
US-08-273- PCT-US95=0 PCT-US95-0 PCT-US93-0 US-08-471-	US-08-471- PCT-US95-1 US-08-471- US-08-471-	US-08-471- US-08-471- US-08-300- PCT-US94-0	US-08-209- US-08-133- US-08-357- US-08-299- US-07-807-	US-08-273- 5480796-8 US-07-807- US-08-299-	5457037-2 US-07-872- 5457037-4 5457037-1
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242 1004 1386 1611 65	66 66 68 68	& & & & & & & & & & & & & & & & & & &	84 84 108 225 225	242 1404 1640 1640	2253 2454 2625 3336
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ALIGNMENTS

Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
C GENERAL INFORMATION:
APPLICANT: SCHEIFINGER, F.
APPLICANT: SCHEIFINGER, F.
APPLICANT: SCHEIFINGER, F.
APPLICANT: FALKNER, F. S.
CORESPONDENCE: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLGY & Lardner
STREET: 1800 Diagonal Road, Suite 500
COUNTRY: USA
STATE: 40A
COUNTRY: USA
ZIT: Alexandria
STATE: WA
COUNTRY: USA
ZIT: Alexandria
STATE: WA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTAM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSSIFICATION NUMBER: US/08/232,463
FILING BAPLICATION NUMBER: US/08/313
FILING DATE:
CLASSIFICATION NUMBER: US/07/935,313 AFLUNCATE:
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY-AGENT INFORMATION:
NAME: BENT, Stephen A.
RECISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECHONIC: (703)836-9300
TELEPHONE: (703)683-4109 US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP. RESULT ~

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single
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: California
                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94105-1493
                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Sar
STATE: Ca
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                     982 GGGCCCCCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCCCCCGGTGTA 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1102 CCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGAGGCTCGTGGAGACCATCTT 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1222 CTACTGGCAAATGCGGCCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTA 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                      922 GGAGGGTGCGCTCTCTGGCACGCGCCACTCCCATCCGTGGGCCGCCAGCACCACCC 981
                                                                                                                                                                                                                                  Gaps
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                                                                                                                        CLONE: pTZgpt-Fls
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                                                                     Query Match 1.8%; Score 67; DB 1; Length 7218; Best Local Similarity 2.4%; Pred. No. 1.46e-25; Matches 9; Conservative 211; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .T 2
US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1282 CGGGGTGCTCCTC 1294
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                                                                                    linear
                                                                             TOPOLOGY: line
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, John M.
APPLICANT: LABAVITCH, John M.
APPLICANT: LABAVITCH, John M.
APPLICANT: POWELL, Ann
APPLICANT: STOTE, Hearli
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1900 TICCCGATGCTGCTGTGTTGTTGTTGTGTGTGCGCACGCTGCACCTCTTGAAGTG 1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1080 CCGCCCCCCCCCTAGTTGACCACGCTGAACAGTGCCTTCACCCTCGAGGTGAGACGCTC 2021
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SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.3%; Score 49; DB 1; Length 7218; 2.0%; Pred. No. 1.85e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Townsend and Townsend Khourie and Crew Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
                                                                                          29,768
FR: 30472/114 IMMU
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APPLICATION NUMBER: EP 91 114.300.6 FILING DATE: 26-AGG-1991 ATTONEZY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
GENERAL INFORMATION:
                                                                                                                      REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                     14:
                                                                                                                                                                                                 TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERICS:
LENGTH: 7218 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 MSSSSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSAN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A: 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 144, Application US/08471052A
Sequence 144, Application US/08471052A
Patent No. 5625033
GENERAL INFORMATION:
APPLICANT: RAY, B. K.
APPLICANT: FOWINES, D. M.
SEQUENCES: 166
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New .c...

CUNTRY: U.5.A.

2.DP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 1; Length 215;
Pred. No. 2.06e-06;
76; Mismatches 95; Indels
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US-08-471-052A-144 STANDARD; DNA; UNC; 66 BP.
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFRENCE/DOCKET NUMBER: 2307E-540
TELEPOMUNICATION INFORMATION:
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1436 TGCTGTGCTGGCGGAGC 1420
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Best Local Similarity 13.2%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
                                                                                                                                                                                                                                                                                                                           single
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CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: DOWELL, Ann
APPLICANT: STOTZ, Henrik
TILLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 HTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTAMTSRNRTGKTANNAVD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :| ::| ::: : : : : : : : | :| :| : | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
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OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP: 15 A: 8 C: 25 G: 26 T: 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 1; Length 215,
Pred. No. 7.21e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                          APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 543-5603
TELEFAX: (415) 543-5603
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
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FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 12.9%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
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94105-1493
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251 GCACGCCGCC 262
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Sequence 142, Application US/08471052A
Sequence 142, Application US/08471052A
Patent No. 5625033
GENERAL INFORMATION:
APPLICANT: Kowy N. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New YOLK
STATE: New YOLK
STATE: New YOLK
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOPPATER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
TILING DATE: 06-JUNE-1995
FTLING DATE: 06-JUNE-1995
FTLING DATE: 06-JUNE-1995
                                                                                                                                                                                               254 CGGCCCCCCCCCCCCCTTCCGCCAGGTGTCCTGCTGCAGGTGTCCTGCAGAAGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 1; Length 69;
Pred. No. 2.91e-01;
18; Mismatches 37; Indels
                                                                                                                                                                               Score 25; DB 1; Length 68;
Pred. No. 2.91e-01;
0; Mismatches 12; Indels
   LENGTH: 68
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
ANTI-SENSE: NO
SEQUENCE 68 BP; 7 A; 38 C; 17 G; 6 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: DNA
SEQUENCE 69 BP; 2 A; 4 C; 6 G; 2 T; 55 OTHER.
                                                                                                                                                                                                                                                                        US-08-471-052A-142 STANDARD; DNA; UNC; 69 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 1101-179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 142:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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Best Local Similarity 11.3%;
Matches 7; Conservative
                                                                                                                Query Match 0.7%;
Best Local Similarity 75.5%;
Matches 37; Conservative
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STRANDEDNESS: single
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1493 GG 1494
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ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Prockop, Darwin J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Williams, Charlene J.
APPLICANT: Williams, Charlene J.
APPLICANT: Ritvaniemi, Pertti
APPLICANT: Baldwin, Clinton
APPLICANT: Hopkinson, Ian
APPLICANT: Ahmad, Nilofer Nina
TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS
NUMBER OF SEQUENCES: 261
                                                                                                                                                                                                                        Score 25; DB 1; Length 66;
Pred. No. 2.91e-01;
18; Mismatches 37; Indels
REFERENCE/DOCKET NUMBER: 1101-179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 709-9090
TELEFAX: 212 869-9864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA
SEQUENCE 66 BP; 2 A; 3 C; 4 G; 2 T; 55 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                 JT 6
US-07-977-284A-243 STANDARD; DNA; UNC; 68 BP.
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CLASSIFICATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 243, Application US/07977284A Sequence 243, Application US/07977284A Patent No. 5558988 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/977,28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,229
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TELECOMMUNICATION INFORMATION:
TELEFHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 243:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                                                                                                                                         / Match 0.7%;
Local Similarity 11.3%;
hes 7; Conservative
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COMPUTER READABLE FORM:
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                                                 Sequence 94, Application PC/TUS9511934
C GENERAL INFORMATION:
C GENERAL INFORMATION:
C TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries NUMBER OF SEQUENCES: 103
C CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
C CITY: New York
C CITY: New York
C COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 100, Application PC/TUS9511934
Sequence 100, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE 1103
CORRESPONDENCE Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match

0.7%; Score 26; DB 2; Length 74;
Best Local Similarity 11.4%; Pred. No. 9.62e-02;
Matches 8; Conservative 19; Mismatches 43; Indels
                                                                                                                                                                                            ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7T 9
PCT-US95-11934-100 STANDARD; DNA; UNC; 74 BP.
                   PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
                                                                                                                                                                                                                                                                                                                                             1101-196-228
                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-:
TELECOMMUNICATION INFORMATION:
TELEFAR: (212) 790-9090
TELEFAR: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2509 CCACCACGCC 2518
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Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                             Score 26; DB 2; Length 74;
Pred. No. 9.62e-02;
20; Mismatches 41; Indels
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Pred. No. 9.62e-02;
19; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP: 6 A: 6 C: 1 G: 1 T: 60 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
                                                                                                                                                                                                                                                               JT 11
PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1101-196-228
                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
         TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
                                                        LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                              Query Match

Best Local Similarity 10.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 11.4%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                 482 GCCCCCAC 475
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                                                                                                                                                                                                                                                                                             Sequence 99, Application PC/TUS9511934
Sequence 99, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE: 103
CORRESPONDENCE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 2; Length 75;
Pred. No. 2.91e-01;
20; Mismatches 43; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 13
PCT-US95-11934-99 STANDARD; DNA; UNC; 75 BP.
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PCT-US95-11934-99 STANDARD; DNA; UNC; 75 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036
COMPUTE READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palcana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-SEP-1995
CLASSIFICATION:
AUTONNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 1101-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEXX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 base pairs
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Best Local Similarity 10.0%;
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STRANDEDNESS: single
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COUNTRY: USA
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US-08-951-733-19.rni

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2449 GAGCTCCTCCCTGAATGAGGCCAGCAGTCTTCGACGTCTTCCTACGCTTCATGTG 2508
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STRATE: New York
CUITY: New York
COUNTY: USA
ZIF: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 10036
COMPUTER: IBM PC-COMPATION:
COMPUTER: 10036
COMPUTER: 10046
COMPUTER: 10056
COMPUTER: 20-SEP-1995
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RIGHT APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICANION:
NAME: Mistock, S. Leslie
REGISTATION NUMBER: 18,872
FREGISTATION NUMBER: 18,872
FREGISTATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                   19; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                               Length 81;
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                             Score 26; DB 2; Louis Pred. No. 9.62e-02;
                                                                              ATORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18 872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.
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PCT-US95-11934-98 STANDARD; DNA; UNC; 81 BP.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 98:
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Best Local Similarity 11.4%;
Matches 8; Conservative
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   0; Gaps
              APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
MUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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Sequence 92, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
WIMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 2; Length 75;
Pred. No. 2.91e-01;
20; Mismatches 43; Indels
                                                                                                                                                                   COUNTRIES 2005

ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934

TITING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER.
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PCT-US95-11934-92 STANDARD; DNA; UNC; 81 BP.
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 75 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.7%;
Best Local Similarity 10.0%;
Matches 7; Conservative
 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 GGCGGCCGTG 252
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我的有种种的人,我们也是有什么,我们也是我们的,我们也是我们的,我们也是我们的,我们也是我们的,我们也是我们的,我们也是我们的,我们也是我们的,我们们们们们们		***************************************
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Dec 24 07:42:45 1998; MasPar time 55.38 Seconds 780.716 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-951-733-20 (1-1154) from US08951733.pep 8624 1 HASGRCVLLRTWEALAPAT.....TALEAAANPALPSDFKTILD 1154 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

116738 segs, 37463448 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir58 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 54.465; Variance 114.185; scale 0.477 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES		
Result No.	Score	Query	Query Match Length DB	DB	ID	Description	Pred. No.
	314	3.6	884	~	553396	telomerase catalytic	1.90e-31
7	162	1.9	099	-	QQBE3	BHLF1 protein - human	4.72e-07
m	153	1.8	504	~	JC1306	virion protein homolo	8.51e-06
4	136	1.6	.240	7	B24264	proline-rich protein	1.59e-03
ς.	141	1.6	276	7	B38965	hypothetical protein	3.53e-04
φ	142	1.6	310	-4	PIHUSD		2.61e-04
7	136	1.6	316	7	S16681	homeotic protein - hu	1.59e-03
ω	137	1.6	628	~	S01955	hypothetical protein,	1.18e-03
σ	129	1.5	264	7	D34768		1.24e-02
10	131	1.5	300	~	S19560	proline-rich protein	6.92e-03
11	126	1.5	302	7	S11790	nodulation protein no	2.92e-02
12	129	1.5	309	~	S10889	proline-rich protein	1.24e-02
13	132	1.5	317	~	A28996	proline-rich protein	5.17e-03
14	127	1.5	266	7	S22933	testis-specific prote	۵.
15	132	1.5	924	7	S27923	gene LF3 protein - hu	Ŋ.
16	131	1.5	1106	7	JQ0405	hypothetical 119.5K p	9
17	130	1.5	1236	7	E70977	hypothetical protein	9.26e-03
18	117	1.4	204	~	A39066		3.53e-01
19	125	1.4	227	~	C29149		3.87e-02
20	123	1.4	240	7	A24264	proline-rich protein	6.79e-02
21	123	1.4	256	~	A60533	tumor-associated anti	6.79e-02
22	118	1.4	322	Н	S00054	nodulation protein no	2.69e-01
23	119	1.4	347	7	S10571	epithelial tumor anti	2.05e-01

1.4 358 1 WMBE38 infected cell protein 1.18e-01 1.4 403 2 535796 osteogenic protein 2.87e-02 1.4 403 2 55796 prpL2 protein - human 6.79e-02 1.4 431 2 509824 hypothetical protein 2.69e-01 1.4 439 2 551939 chitimase (EC 3.2.1.1 6.79e-02 1.4 515 2 510572 epithelial tumor anti 2.05e-01 1.3 202 2 B36795 protein protein 7.86e-01 1.3 202 2 B36795 protein protein 7.86e-01 1.3 202 2 B36795 proline-rich protein 7.86e-01 1.3 202 2 B36795 proline-rich protein 7.86e-01 1.3 202 2 B36795 proline-rich protein 7.86e-01 1.3 270 2 E23373 proline-rich protein 7.86e-01 1.3 295 2 B48013 proline-rich protein 7.86e-01 1.3 321 1 A28663 nodulation protein 0.38e-01 1.3 321 2 55545 hypothetical protein 7.86e-01 1.3 378 2 JC5707 HYA22 protein - human 6.03e-01 1.3 378 2 A56186 cyclin E - African cl 7.86e-01 1.3 704 2 A3041 synapsin Is - rat 1.02e+00 1.3 1255 2 B33175 epislalin B - human 1.02e+00 1.3 3149 1 QOBE8 BPLFI protein - human 6.03e-01	S53396 #type complete telomerase catalytic chain EST2 - yeast (Saccharomyces cerevisiae) S protein L8943.12; protein YLR318w #formal_name Saccharomyces cerevisiae 05-May-1995 #sequence_revision 01-Sep-1995 #text_change S53396	S533 Du, Subm Subm The S533 L_type iferen sntal_	12R #length 884 #molecular-weight 1 3.6%; Score 314; DB 2 larity 24.3%; Pred. No. 1.90e- Conservative 122; Mismatches	PKI : SSI	LLKKLRLKDFRWLFIS-DIWFTKHNFENLNQLAIC-FISWLFRQLIPKIIQTFFYCTEIS 387 	VIIVYE-RHDTWNKLITPFIVEYFKTY-LVE-NNV-CRNHNSYTLSNFNHSKMRIIPK 443 	NNEFRIJAIPCRGADEBEFTIYKENHK-NA-IQPTQKILEYLRNKRPTSF-TKIYSPT 500 	ADRI-KEFKORLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMR-ILKDALKNENGFF 558
111111111111111111111111111111111111111	1 NAME	ssion ption sion sidu css- peri	posit Match Acal	271 LSHLSRQS : 470 LVQLLRQH	330 LLKKLR : 530 LTWKMS	388 STVTI 590 FQKNR	444 KSNNEFI :: 649 -PDGLRI	501 QIADRI : 707 DI-HRA
40000010040000000000000000000000000000	RESULT ENTRY TITLE ALTERNATE ORGANISM DATE	REFERENCE #authot #authot #access #access ### ### ### ### GENEDICS #### ###############################	#map_ SUMMARY Query Best I Matche	g čo	og og	oy oy	oy oy	Dp Qy

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##molecule_type DNA
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                                                              #journal
#title
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REFERENCE
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                                                                                                                                                                                                                                                                                       COMMENT
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#journal Mol. Biol. Med. (1983) 1:21-45
#title Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8
Epstein-Barr virus.
#cross-references MUID:85035713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.;
Farrell, P.J.; Gibson, T.J.; Hatfull, G.; Hudson, G.S.;
Satchwell, S.C.; Seguin, C.; Tuffnell, P.S.; Barrell, B.G.
Nature (1984) 310:207-211
DNA sequence and expression of the B95-8 Epstein-Barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 162; DB 1; Length 660;
Pred. No. 4.72e-07;
34; Mismatches 60; Indels 14; Gaps 12;
                                                              E----M-EIF-K-T---ALWVEDKCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKAS 658
                                                                                                                                                                                                                                                                                                                            GPPPTRSGAAAQ-RTHRRPPGCPRSARNPGCPRTWRR--R-SGAQRGHPPPGAGQRPSGP 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BHLF1 protein - human herpesvirus 4 (strain B95-8)
#formal_name human herpesvirus 4, Epstein-Barr virus
25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change
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virion protein homolog - bovine herpesvirus 1
alpha TIF; BHV-1 protein homolog; ICP25; Vmw65; VP16
#formal_name bovine herpesvirus 1
05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #cross-references MUID:84270667
#contents annotation; protein coding region
MAENT The sequence contains four perfect repeats (residues 149-273, 274-398, 399-523, and 524-648).
ASSIFICATION *superfamily human herpesvirus 4 BHLF1 protein #length 660 #molecular-weight 66244 #checksum 8900
                                                                                                                                                                                        VRSQY-FFNTINT-G-VLKLFNV-VNASRVPKPY-ELYIDNVR-TVHLSNQDVIN---VV-
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Matches 48: Control of the control of
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#authors Ann, D.K.; Carlson, D.M.
#journal J. Biol. Chem. (1985) 260:15863-15872
#title The structure and organization of a proline-rich protein gene of a mouse multigene family.
#cross-references MUID:86059475
                                                                                                                                                                             ##cross-references EMBL:211610; NID:91065725; PID:e264419; PID:91065726
This protein interacts with cellular transcription factors to transactivate immediate early viral genes.
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hypothetical protein B - Enterobacter agglomerans insertion
                                                       herpes
(UL48).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 APAEAGGGWRRSGSTRTRGRAARSTTGRLQRPCCGPRRRAKC-CRATP-RQRLR--ARGE 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRHTS-GSGAFSQ-GRRPGRVCRLGWACKARSGPARGCPGPSPVRSGLGLSR-ARGSPGP 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 PPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAAPE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B24264 *type fragment
proline-rich protein MP3 - mouse (fragment)
*formal_name Mus musculus *common_name house mouse
09-sep-1987 *sequence_revision 09-sep-1987 *text_change
03-May-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                  *superfamily herpesvirus alpha trans-inducing protein DNA binding; transcription regulation #length 504 #molecular-weight 54028 #checksum 8743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 VNGSQQGPPPPGGPQPRPPGGPQPRPPGGPQPPPPGGPQPRPPQGPPPGGPQPRP
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Carpenter, D.E.; Misra, V. Gane (1992) 119:259-263 Sequences of the bovine herpesvirus 1 homologue of simplex virus type-1 alpha-trans-inducing factor
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 153; DB 2; Length 504;
Pred. No. 8.51e-06;
33; Mismatches 56; Indels 12;
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Pred. No. 1.59e-03;
38; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #superfamily proline-rich protein
#length 240 #checksum 5152
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Best Local Similarity 27.2%;
Matches 41; Conservative
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Best Local Similarity 31.3%;
Matches 46; Conservative
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US-08-951-733-20.rpr

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cession D25372
##molecule_type_mRNA
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                                                                   Steibl, H.D.; Lewecke, F.M.
Gene (1995) 156:37-42
ISIZ2: analysis and distribution of a new insertion sequence
in Enterobacter agglomerans 339.
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#journal J. Blol. Chem. (1985) 260:11123-11130
#title Differential RNA splicing and post-translational cleavages in the human salivary proline-rich protein gene system.
#cross-references MUID:85289325
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salivary proline-rich glycoprotein precursor PRB4 (large saliele) - human
basic proline-rich protein IB-5; proline-rich peptide P-D #formal_name Homo sapiens #common_name man
19.Feb-1984 #sequence_revision 12-Apr-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Lyons, K.M.; Stein, J.H.; Smithles, O.
#Journal Genetics (1988) 120:267-278
#title Length polymorphisms in human proline-rich protein genes
generated by intragenic unequal crossing over.
#cross-references MUID:89121440
                                                                                                                                                                                                                                                                                                                                                                                                                                       42 ITELALERRR-FGYRR-IWQLLRREGLHVNHKRVYRLYHLSGLGVKRRRR-RKGLATERL 98
                #formal_name Enterobacter agglomerans
03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change
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MARY #length 276 #molecular-weight 31718 #checksum 3927
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Pred. No. 3.53e-04;
23; Mismatches 30; Indels
                                                                                                                                                                                                                              ##molecule_type DNA
##residues 35-36,'E',38-112,155-310 ##label LY2
##cross-references EMBL:X07704
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#fresidues 1-10 c ...
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##note large allele
cession $03175
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S10890
sequence IS1222
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Best Local Similarity 33.7%;
Matches 30; Conservative
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A38965
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S62891
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#authors Saitoh, E.; Isemura, S.; Sanada, K.
#Journal J. Biochem. (1983) 93:495-502
#title Complete amino acid sequence of a basic proline-rich peptide,
P.D. from human parotid saliva.
#cross-references MuID:83186122
#accession A01295
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Chorald, C.J.; Williamson, M.P.
Tannin interactions with a full-length human salivary proline-rich protein display a stronger affinity than with single proline-rich repeats.
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#product proline-rich peptide P-D #status experimental #label MAT\
#binding_site carbohydrate (Asn) (covalent) #status experimental\
                                                            #authors Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
#journal Biochemistry (1991) 30:3351-3356
#title Basic proline rich proteins from human parotid saliva:
    relationships of the covalent structures of ten proteins
#cross-references MUID:91190884
#accession E38355
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J. Biochem. (1983) 93:857-863
Amino acid sequences of glycopeptides obtained from basic
proline-rich glycoprotein of human parotid saliva.
A61294
1-36,'E', 38-112,'T', 114-115,'P',117-121,185-271,'A',
273-310 ##label MAE
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#length 310 #molecular-weight 31351 #checksum 3960
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##molecule_type protein
##residues 54-57,'E',59-73,'R';82-101 ##label SHI
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##residues 241-254,'KN',257-310 ##label KAU
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##residues 241-310 ##label SAI
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##residues 241-252 ##label CHA
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Best Local Similarity 25.0%;
Matches 73; Conservative
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Nuclet. Acids Res. (1988) 16:157-6173
Overlapping open reading frames revealed by complete
nucleotide sequencing of turnip yellow mosaic virus genomic
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Library, January 1991
#superfamily unassigned homeobox proteins; homeobox homology
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hypothetical protein, 69K - turnip yellow mosaic virus
#formal_name turnip yellow mosaic virus, TYMV
21.NOV-1993 #sequence_revision 26-May-1995 #text_change
24-Sep-1998
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Pred. No. 1.59e-03;
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                                                          APPAGKPQGPPPPPQGGRPPRP 302
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##molecule_type genomic RNA
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Best Local Similarity 30.9%;
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281 PGRTRGPS 288
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#title Gene sequence of mouse B-type proline-rich protein MP4.
Transcriptional start point and an upstream phylogenetic footprint with ets-like and rel/NFKB-like elements.
#cross-references MID:92111548
#accession S19560
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#title Sequence analysis of the inverted terminal repetition in genome of the parapoxvirus, orf virus.
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                                                            Gaps
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ORF4 protein - Orf virus (strain NZ2)
#formal_name Orf virus
23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change
31-Oct-1997
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#formal_name Mus musculus #common_name house mouse
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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Pred. No. 1.24e-02;
40; Mismatches 37; Indels
Pred. No. 1.18e-03;
64; Mismatches 134;
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Best Local Similarity 28.2%;
Matches 33; Conservative
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S19560
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#journal Mol. Microbiol. (1990) 4:921-932
#title Analysis of three nodD genes in Rhizobium leguminosarum
biovar phaseoli; nodDl is preceded by nolE, a gene whose
product is secreted from the cytoplasm.
#cross-references MUID:91014692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 IREALQHIRLNIIPWDKFTPDQSDRHFR-VS-LCDFVTVVLFQKILERLAREAPGISFDL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 PGNQQGPPPQG-GPQQRPP-QPGNQQGPPPGGPQQRPPQPGGNQGGPP-QGGPHP-PPR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 PGNQQGPPPQGGPQQRPTQPGNQQGPPQQGG-PQAPPRPGNQQGPPPQGPPRTGNQQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 RGAAPEPERTPVGQGSWAHPGRIRGPSDRGFCVVSPARPA-EEAISLEGALSGIRHSHPS 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 LLRTWEALAPATP-AMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPA 67
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#formal_name Rhizoblum leguminosarum bv. phaseoli
21-Nov-1993 #sequence_revision 13-Jan-1995 #text_change
16-Feb-1997
                                                                                                    #authors Roberts, S.G.E.; Layfield, R.; McDonald, C.J.
#journal Nucleic Acids Res. (1991) 19:5205-5211
#title The mouse proline-rich protein MP6 promoter binds isoprenaline-inducible parotid nuclear proteins via highly conserved NFkB/rel-like site.
#cross-references MUID:92020206
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DNA binding; transcription regulation
#length 302 #molecular-weight 34274 #checksum 3819
                                                                                                                                                                                                                                                                                                                            *superfamily proline-rich protein
*length 300 *molecular-weight 31129 *checksum 8443
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Pred. No. 2.92e-02;
28; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 6.92e-03;
40; Mismatches 54; Indels
                                    ##residues 1-300 ##label ROB
##cross-references GB:X58438; NID:953181; PID:953182
                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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##cross-references EMBL:X61126
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preliminary
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Best Local Similarity 25.2%;
Matches 34; Conservative
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Best Local Similarity 31.4%;
Matches 38; Conservative
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VGRQHHAGPPSTSRP 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 GPPP-QGGNQSQG-PPPHPGKPEGPPP-QGG-NQSQGPPPRP-GKPE-GPPPQGGNQSQG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 -P-PPRPGKPEGPPPQGGNQSQGPPPRPGKPEGPPPQGGNQSQGPPPRPGKPEGSPSQGG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #product proline-rich protein M14 #status predicted
#label MAT
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proline-rich protein M14 precursor - mouse
#formal_name Mus_musculus #common_name house mouse
30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
20-Mar-1998
proline-rich protein - human #formal_name man 07-oct-1994 #sequence_revision 26-May-1995 #text_change 08-Sep-1997
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J. Biol. Chem. (1988) 263:10887-108987-10898
Molecular evolution of the mouse proline-rich protein multigene family. Insertion of a long interspersed r
                                                                                                                                                                                                                                                                                                                                                     22/1; 34/1
#superfamily proline-rich protein
#length 309 #molecular-weight 30936 #checksum 3043
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                                                                                                                                    #authors Lyons, K.M.; Stein, J.H.; Smithles, O.
#journal Genetics (1988) 120:267-278
#title Length polymorphisms in human proline-rich prot
generated by intragenic unequal crossing over
#cross-references MUID:89121440
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 309
                                                                                                                                                                                                                                                                                         ##residues 1-309 ##label LYO ##cross-references EMBL:X07881; NID:935637; PID:9296669
                                                                                                                                                                                                                                                       preliminary; translation not shown
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Pred. No. 1.24e-02;
38; Mismatches 53;
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#accession A28996
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Best Local Similarity 30.4%;
Matches 45; Conservative
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#authors Mazarakis, N.D.; Nelki, D.; Lyon, M.F.; Ruddy, S.; Evans, E.P.; Freemont, P.; Dudley, K. #journal Development (1991) 111:561-571 fittle Isolation and characterisation of a testis-expressed developmentally regulated gene from the distal inversion of the mouse t-complex. #cross-references MID:91372153 #accession $22933
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submitted to the EMBL Data Library, August 1990
Sequence and transcription of Raji Epstein-Barr virus DNA
Spanning the B95-8 deletion region.
                                                                                      95 PPPGGPQPRPPGGPPPFGG-PQPRPPQGPPPFGGPQPRPPGGPPPFGGPQQRPPPP 153
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                                                            37 SGSQPRPPVNGSQQGPPPPGGPQPRP-PQGPPPPGGPQPRPPQGPPPPGGPQPRP-PQGP 94
                                                                                                                                                                                                                                                                                                     testis specific protein Bs13 - mouse
formal_name Mus musculus #common_name house mouse
22.Nov-1993 #sequence_revision 10-Nov-1995 #text_change
10-Sep-1997
$222933
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Parker, B.D.; Bankier, A.; Satchwell, S.; Barrell, B.;
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#accession 5229.3
##molecule_type mRNA
##residues 1-566 ##label MAZ
##cross-references EMBL:X52128; NID:954852; PID:954853
#fcross-references EMBL:X52128; NID:954852; PID:954853
#fcross-references EMBL:X52128; DID:954853
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##cross-references EMBL:M35547; NID:g330420; PID:g330421
Y #Length 924 #molecular-weight 94304 #checksum 8997
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Best Local Similarity 35.7%; Pred. No. 2.19e-02;
Matches 30; Conservative 19; Mismatches 30; Indels
Pred. No. 5.17e-03;
38; Mismatches 64; Indels
                                                                                                                                                                                                                                                   318 HPSVGRQHHAGPPSTSRPPRDTPCPP 345
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                                                                                                                                                                                                                           154 GGPQPRPPQGPPPAGPQPRPPQGPPPP 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 VSPARPAEEATSLEGALSGIRHSH 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type DNA
##residue
Best Local Similarity 26.4%;
Matches 39; Conservative
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Dec 24 07:48:22 1998; MasPar time 38.16 Seconds 811.688 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-951-733-20 (1-1154) from US08951733.pep 8624

Title: Description: Perfect Score: Sequence:

1 HASGQRCVLLRTWEALAPAT.....TALEAAANPALPSDFKTILD 1154

PAM 150 Gap 11 Scoring table:

74019 segs, 26840295 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot35 1:swissprot

Mean 55.898; Variance 96.260; scale 0.581 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	4.64e-09	1.47e-07	4.56e-07	8.72e-06	5.26e-05	2.15e-04	4.31e-04	2.37e-03	1.69e-03	3.32e-03	1.25e-02	3.30e-02	3.32e-03	3.30e-02	3.32e-03	3.30e-02	1.17e-01	6.23e-02	8.54e-02	5.40e-01	1.17e-01	5.40e-01	8.54e-02
Description	HYPOTHETICAL BHLF1 PRO	ALPHA TRANS-INDUCING P	SALIVARY PROLINE-RICH	SALIVARY PROLINE-RICH	69 KD PROTEIN.	SALIVARY PROLINE-RICH	PROLINE-RICH PROTEIN M	NODULATION PROTEIN D I	TESTIS-SPECIFIC PROTEI	PROLINE-RICH PROTEIN M	NODULATION PROTEIN D I	BONE MORPHOGENETIC PRO	BONE MORPHOGENETIC PRO	HYPOTHETICAL PROTEIN U	MESENCHYME FORK HEAD P	REGULATORY PROTEIN E2.	HYPOTHETICAL GENE 1 PR	TRNA-(MS[2]IO[6]A)-HYD	HYPOTHETICAL 29.3 KD P	NODULATION PROTEIN D3.	NODULATION PROTEIN D I	MATING TYPE PROTEIN A-	SALIVARY PROLINE-RICH
e e	YHL1_EBV	ATIN_HSVBP	PRPM_HUMAN	PRPL_HUMAN	V70K_TYMV	PRP4_HUMAN	PRP3_MOUSE	NOD3_RHILP	TS13_MOUSE	PRP2_MOUSE	NOD1_RHISN	BM8A_MOUSE	BMP8_HUMAN	UL61_HCMVA	MFH1_HUMAN	VE2_HPV05	VG01_HSVEB	MIAE_SALTY	Y091_NPVOP	NDO3_RHILO	NOD1_BRAJA	MATD_NEUCR	PRP1_HUMAN
DB	; -	-1	-	-	-	-	-	-	H	Н	-	Н	н	Н	—	-		-	-		-	-	-
Length	999	504	234	276	628	247	296	302	266	261	325	399	402	431	501	514	202	270	279	301	321	324	331
% Query Match	1.9	1.8	1.7	1.6	1.6	1.5	1.5	1.5	1.5	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.3	1.3	1.3	1.3	1.3	1.3	1.3
Score	162	153	150	142	137	133	131	126	127	125	121	118	125	118	125	118	114	116	115	109	114	109	115
Result No.	-	7	æ	4	S	ø	7	∞	σ	10	11	12	13	14	15	16	17	18	19	. 50	21	22	23

1.17e-01 3.99e-01 2.95e-01 1.59e-01 1.59e-01 1.59e-01 1.78e-01 1.78e-01 1.39e-01 1.39e-01 1.39e-01 1.39e-01 1.39e-01 1.39e-01 1.36e-01 1.31e+00 1.39e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01 1.36e-01				IRINAE.	ئ.'. بن			Gaps 12;	SGP 306	: : GGS 249	RLP 364 SLE 308			
G1/S-SPECIFIC CYCLIN E G1/S-SPECIFIC CYCLIN E G1/S-SPECIFIC CYCLIN E G1/S-SPECIFIC CYCLIN E REGULATORY PROTEIN E2. REGULATORY PROTEIN E2. 69 KD PROTEIN. PROLINE-RICH PROTEIN L SYNAPSINS IA AND IB. SYNAPSINS IA AND IB. SYNAPSINS IA AND IB. HYDOTHETICAL TRANSCRIP HYPOTHETICAL		60 AA.	E UPDATE) ION UPDATE) (HUMAN HERPESVIRUS 4).	PESVIRIDAE; GAMMAHERPESV	DEININGER P.L., FARRELL P., , SATCHWELL S.C., SEGUIN C	REPEAT. AA TANDEM REPEATS.	.5 CRC32;	DB 1; Length 660; 4.64e-09; tches 60; Indels 14;	R-SGAQRGHPPPGAG	-LGCERAWNHSVREAGVPLGLPAPGA-RRRGG	TGGRPAAPGAPGTPAAPGPGGGAAVPSGATPHPERGSGPADPPAAARLPPERQEPRLP :: :	GCP 397	 PCP 344	504 AA.
CGEL_XENLA CGEZ_XENLA VEZ_HPV0B VEZ_HPV36 VEZ_HPV36 VY0Z_HPV36 VY0Z_HYW70 LA17_YEAST SYNL_RAT	ALIGNMENTS	PRT; 6	ED) SEQUENC ANNOTAT B95-8)	IRUSES;	IN M.D., bSON G.S., ; TED_CDS.	PROTEIN;	ω	Score 162; Pred. No. 4 34; Mismat	PPPTRSGAAQ-RTHRRPPGCPRSARNPGCPRTWRR	-PRR-R-LGCER	TGGRPAAPGAPGTPAAPGPGGGAAVPSGATPHPERGSGPADPP :: :	AQRTHR-	::::: : :: : GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCP	PRT;
адааааааааааааааа			CREATED) LAST SEQ LAST ANN TEIN. RAIN B95	В	BIGC HI B.G.	EARLY	4	.98; .88; 1ve	Spage	IASG	PGG(PER:	SGA	:: : HAGPI	D; CREATED)
4008 4008 4008 5009 5009 5009 5009 5009 5009 5009 5		STANDARD	01, 01, 36, 1 PRO S (ST	NVELOF	N.A. 0667. IER A.T., BIGG HATFULL G., HU , BARRELL B.G. 7.211(1984). -; NOT_ANNOTA'	3. EIN; E 648	273 398 523 648 ; 662	1 30 rvat	-RTHRF	ARPPPE	TPAAPC RGAAPE	GPPPTF	VGRQHI	STANDARD L. 25, C
				Ø	E FROM N.A. ; 84270667. ; BANKIER A.T., F. I.J., HATFULL G., L. P.S., BARELL I. 310.207-211(1984) 01555; -; NOT_ANN	11 "	149 274 399 524 660 AA	Similarity 48; Conserv	RSGAAAQ	PPLYQLGAATQARPPHASG	AAPGAPG : PLPKRPR	AQRC-PA	::: : TRHSHPS	(RE
1114 1111 1111 1111 1111 1111 1111 111		1 1_EBV	21-JUL-1986 (R 21-JUL-1986 (R 21-JUL-1998 (R 15-JUL-1998 (R HYPOTHETICAL B	IDAE; D	LINE SEQUENCE FR MEDLINE; 84 BAER R., BA GIBSON T.J. TUFFNELL P. NATURE 310:	PIR; A03742; HYPOTHETICAL DOMAIN	REPEAT REPEAT REPEAT REPEAT SEQUENCE	Match ocal s	ტ -	4 GPPLY	۰ 0	5 0	S	LT 2 ATIN_HSVBP P30020; 01-APR-1993
40000000000000044444440000000000000000		ïΛ						Query } Best LA Matche	251	19	30	36	30	SO
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(FRAGMENT).
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PRPL_HUMAN
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      88
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                                                                                                                                                                  351 APAEAGGGWRRSGSTRTRGRAARSTTGRLQRPCCGPRRRAKC-CRATP-RQRLR--ARGE 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIF).
BOUTNE HERRESYLKUS TYPE I (STRAIN P8-2).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 PRHTS-GSGAFSQ-GRRPGRVCRLGWACKARSGPARGGPGPSPVRSGLGLSR-ARGSPGP 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRPM_HUMAN STANDARD; PRT; 234 AA.
P10161; P02813;
01-MR=1989 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) (CONTAINS: PEPTIDE P-D)
                                                                                                                                                                                                                                                                                                                                                                                                             / Match 1.8%; Score 153; DB 1; Length 504; Local Similarity 31.3%; Pred. No. 1.47e-07; nes 46; Conservative 33; Mismatches 56; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 150; DB 1; Length 234;
Pred. No. 4.56e-07;
41; Mismatches 53; Indels 10;
                                                                                                                                                                                                                                                                                                                                               TRANSCRIPTION REGULATION; TRANS-ACTING FACTOR; DNA-BINDING SEQUENCE 504 AA; 54028 MW; 79F42020 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT: PAROTID GLAND: SALIVA; MULTIGENE FAMILY. NON_TER egin{array}{c} 1 & 1 \\ 1 & 1 \\ \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 PEPTIDE P-D.
23676 MW; ED2D4ADC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 QHHAGPPSTSRPPRPWDTPCPPVYAET 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 GPACGGPSRARGGRRRASPANP-FGGT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMITHIES 0.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SANADA K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE: 83186122.
SAITOH E. ISEMURA S., SANADA
J. BICCHEM. 93:495-502(1983).
EMBL; X07704; E265547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 1.7%;
Local Similarity 29.3%;
nes 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 89121439.
LYONS K.M., STEIN J.H., SM
GENETICS 120:255-265(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A03295; PIHUSD.
PIR; S03175; S03175.
HSSP; P19999; 1CLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 165-234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 AA;
                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 93012995
                                                                                                                                                       93012995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 168730; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 RPRRGAAPEPERTPVGQGSWAHPGRTRGPSDR-GFCVVSPARPAE-EATSLEGALSGTRH 316
GPPP-QGGNQSQG-PPPHPGKPERPPP-QGG-NQSHRPPPPP-GKPER-PPPQGGNQSQG 141
                                                                                                                 134 QGGNQSQG-PPPHPGKPERPPP-QGG-NQSHRPPPPP-GKPER-PPPQGGNQSQG-P-PP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 HPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPFGKPQGPPPGGNPQQPQ 246
                                                                                                                                                                                                                                                                                                                                  P10162; P02813;
01-MR-1989 (REL. 10, CREATED)
01-MR-1989 (REL. 30, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) (CONTAINS: PEPTIDE P-D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                            <u>ئ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6%; Score 142; DB 1; Length 276
28.2%; Pred. No. 8.72e-06;
tive 41; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESULT 5

D V70K_TYMV STANDARD; PRT; 628 AA.

C P10357;
T 01-MAR-1989 (REL. 10, CREATED)
T 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
T 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
S KD PROTEIN.
T OTRNIP YELLOW MOSAIC VIRUS.
TURNIP YELLOW MOSAIC VIRUS.

VIRIDAE; SS-RNA NONENVELOPED VIRUSES; TYMOVIRIDAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT; PAROTID GLAND; SALIVA; MULTIGENE FAMILY.
NON-TER
207 77 77 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDE P-D.
; 4838945A CRC32;
                                                                                                                                                                                                                                                                                                                      276 AA
                                                                                                                                                                               200 PQQPQAPPAGKPQGPPPPPQGGRPPRP 226
                                                                                                                                                                                                         312 SGTRHSHPSVGRQHHAGPPSTSRPPRP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMITHIES O.;
                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 PER
; 27816 MW; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 SHPSVGRQHHAGPPSTSRPPRP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 APPAGKPQGPPPPPQGGRPPRP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAITOH E., ISEMURA S., SANADA F. J. BIOCHEM. 93.495-502(1983).
EMBL; X07715; E4806; ALT_SEQ. PIR; A03295; PIRUSD.
PIR; S03176; S03176.
HSSP; P19999; LCLG.
MIM; 180990; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 28.2%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 89121439.
LYONS K.M., STEIN J.H., SM
GENETICS 120:255-265(1988)
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 207-276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 AA;
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PPP-QGGNQSQGTPPPPGK-PERPPP-QGG-NQSHRPPPPP-GKPER-PPPQGGNQSQG- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT; SALIVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RHIZOBIACEAE
                                                                                                                                                                                                                                                                                            7
PRP3_MOUSE
P05143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOD3_RHILP
P23720;
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SEQUENCE
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110
PRESULT
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                                                                                                                                                                                                                                                                                       Gaps 20;
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                                                                                                                                                                                                                                                                                                                                                           308 EG-ALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLY-SSGDKEQLRP 365
                                                                                                                                                                                                                                                                                                                              157 GPVLTETKPRTSVRQPRSATRGPSFRPILLPKV-VH-VHDDPPHSSLRPRGSRSRQLQPT 214
                                                                                                                                                                                                                                                                                                                                                                                                                           215 VRRPLLAPNQFHSPRQPPPLSDDPGILGPRPLAPHSTRDPPRPI-TPGPSN-THDLRPL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 ASRSLPLPKRPRRGAAPEPERTPVG-QGSWA-HPGRTRGPSDRGFCVVSPARPAEEATSL 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 SSIRKDALLQTGPRLGHLERLGQPANLRTSERSPPTKRRLPRSSEPNRLPKPLPEATLAP 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 SFLL-SSL-R--PSLTGARRIVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLG- 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 SVLPRISPRRGLLPNPRRHRISTGHIPPITISRPIGPPSRLQRPVH-LYQSSPHIPNFRP
                                         MORCH M.D., BOYER J.C., HAENNI A.L.;
NUCLEIC ACIDS RES. 16:6157-6173(1988).
-!- FUNCLION: NOT KNOWN.
-!- SIMILARITY: TO 65 TO 70 KD PROTEIN FROM OTHER TYMOVIRUSES.
EMBL; X07441; G62223; ALT_SEQ.
PIR; S01955; S01955.
SEQUENCE 628 AA; 9E64ED49 CRC32;
                                                                                                                                                                                                                                   Score 137; DB 1; Length 628;
Pred. No. 5.26e-05;
64; Mismatches 134; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 133; DB 1; Length 247;
Pred. No. 2.15e-04;
40; Mismatches 56; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 SYRHRRPYPLLPNPPAALPSIAYTSSRGKIHHSLPKGALPK-EGAPPPPRRL 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRP4_HUMAN STANDARD; PRT; 247 AA.
P10163; P02813;
21-JUL-1986 (REL. 01, CREATED)
13-MGG-1997 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYCOSYLATED PROTEIN
MISSING (IN REF. 2).
D -> A (IN REF. 2).
62BE90BB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAEDA N., KIM H.-S., AZEN E.A., SMITHIES O.;
J. BIOL. CHEM. 260:11123-11130(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN N1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE, 89121440.
LYONS K.M., STEIN J.H., SMITHIES O.
GENETICS 120:267-278(1988).
EMBL; K03207; G199508; -.
HSSP; R19999; ICLG.
MIM; 168730; -.
MIM; 180990; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
39 PI
177 GI
57 MI
218 D
25108 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5%;
                                                                                                                                                                                                                                      Query Match 1.6%;
Best Local Similarity 25.0%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 AA;
SEQUENCE FROM N.A. MEDLINE; 88289359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 85289325.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT;
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  SHRCCRRRR
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Gaps

40; Conservative

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74 PPPGGPQPRPPQGPPPPGG-PQPRPPQGPPPPGGPQQRPPPGGPQGRPPQGPPPP 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 SGSQPRPPVNGSQQGPPPPGGPQPRP-PQGPPPPGGPQPRPPGGPQPRP-PQGP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAVIS E.O., JOHNSTON A.W.B.;
MOL. MICROBIOL. 4:921-932(1990).
-!- FUNCTION: NODD REGULATES THE EXPRESSION OF THE NOD ABCFE GENES
WHICH ENCODE OTHER NODDILATION PROTEINS. NODD IS ALSO A NEGATIVE
REGULATOR OF ITS OWN EXPRESSION. BINDS FLAVONOIDS AS INDUCERS.
195 PPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSL
                                                                                       P-PPHPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPAGGNP
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.5%; Score 131; DB 1; Length 296;
llarity 26.4%; Pred. No. 4.31e-04;
Conservative 38; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
296 AA; 29521 MW; C61DDCC6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
10-CT-1994 (REL. 30, LAST ANNOTATION UPDATE)
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
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01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
NODULATION PROTEIN D III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 GGPQPRPPQGPPPAGPQPRPPQGPPPP 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANN D.K., CARLSON D.M.;
J. BIOL. CHEM. 260:15863-15872(1985).
EMBL; M12100; G200549; -.
HSSP; P19999; ICLG.
                                                                                                                                                                                                                                                                                                                                     314 TRHSHPSVGRQH-HAGPPSTSRPPRP 338
                                                                                                                                                                                                                                                                                214 QQPQDPPAGKPQGPPPPPGGGRPPRP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Matches 39; Conser
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94 VTRGAPLPPSPG-KGHLGGTPSSH 116
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AC PR
AC PO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 IREALQHIRLNIIPWDKFTPDQSDRHFR-VS-LCDFVTVVLFQKILERLAREAPGISFDL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 LMIERNLTAAARSINLSQPAMSAAVRRL-RSYFRDEL-FTMRGREFVPTP-R-AEDLAPA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 SARGIDRVGSTVARARPPSPQGPRRGAVKTAPRGPVGHGGLRTGPTSRCPQPSARAKLPS 93
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAZARAKIS N.D., NELKI D., LYON M.F., EVANS E.P., RUDDY S., FREEMONT P., DUDLEY K.; DEVELOPMENT 111:561-571(1991).
-!- FUNCTION: POSSIBLY PLAYS AN IMPORTANT ROLE IN SPERM DEVELOPMENT AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                        EMBL; X54215; G46237; -.
PIK; S11790.
PRIS, S11790.
NODULATION: TRANSCRIPTION REGULATION; DNA-BINDING; ACTIVATOR; REPRESSOR; PLASMID.
DNA.BIND
DNA.BIND
SEQUENCE 302 AA; 34274 MW; ED62D2FA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: TESTIS.
-!- DEVELOPMENTAL STAGE: FIRSTLY EXPRESSED IN THE PACHYTENE SPERMATOCYTE STAGE.
-!- SIMILARITY: SOME TO YEAST SOKI.
EMBL: X52128; G54833; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 127; DB 1; Length 566;
Pred. No. 1.69e-03;
19; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                   Length 302;
                                                                                                                                                                                                                                                                                                                Score 126; DB 1; Length 302
Pred. No. 2.37e-03;
28; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; S2293; corrections of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7A421F03 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
TESTIS-SPECIFIC PROTEIN PBS13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   566 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRR 1.
LRR 2.
LRR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61970 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CBA/CA; TISSUE-TESTIS; MEDLINE; 91372153.
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 31.4%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 35.7%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440
298
298
305
312
566 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S22933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
ID TS13_MOUSE
AC Q01755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 L 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239
STREETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 음
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 РРОСРРРЕССРОРКРРОСРРРЕССРОРКРРОСРРРЕССРООКРРОСРРЕСРОВЕРРОС 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 РРРРGGPQLRPPQGPPPAGP-QPRPPQGPPPAGPQPRPPQGPPTTGPQPRPTQGPPPT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERRET X.;

NATURE 387:394-401(1997).

INTURE 387:394-301.

INTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 97305956.
FREIBERG C.A., FELLAY R., BAIROCH A., BROUGHTON W.J., ROSENTHAL A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLASMID SIM PNGR234A.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.4%; Score 125; DB 1; Length 261; 7.0%; Pred. No. 3.32e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROLINE-RICH PROTEIN MP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9D830DAF CRC32;
                                                                                                                                                                                                                                                                                                                                      13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Mismatches
                                                                                                                                                                                                                                                261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 86659475.
ANN D.X., CARLSON D.M.;
J. BIOL, CHEM. 260:15863-15872(1985).
EMBL; M12099; G200547; -..
HSSP; P19999; 1CLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 GGPQQQPPQGPPPGGPQPRPPQGPPPP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 VGRQHHA--GPPSTSRP-PRPWDTPCPP 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROLINE-RICH PROTEIN MP-2 PRECURSOR
                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHIZOBIUM SP. (STRAIN NGR234).
295 VSPARPAEEATSLEGALSGTRHSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 AA; 26034 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 27.0%;
les 40; Conservative
                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT; SALIVA; SIGNAL. SIGNAL 1 15 CHAIN 16 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NODULATION PROTEIN D I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NODD1 OR Y4AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHIZOBIACEAE
                                                                                                                                                                                     LT 10
PRP2_MOUSE
P05142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOD1_RHISN
P55359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
BONE MORPHOGENETIC PROTEIN 8 PRECURSOR (BMP-8) (OSTEOGENIC PROTEIN 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 90269039.
CHEE M.S., BANKIER A.T., BECK S., BOHNI R., BROWN C.M., CERNY R.,
CHEE M.S., BANKIER A.T., BECK S., BOHNI R., BROWN C.M., CERNY R.,
HORSNELL T., HUTCHISON C.A. III, KOUZARIDES T., MARTIGNETTI J.A.,
PREDDIE E., SATCHWELL S.C., TOMLINSON P., WESTON K.M., BARRELL B.G.;
CURR. TOP. MICROBIOL. IMMUNOL. 154:125-169(1990).
EMBL, X17403, E27260;
PIR: S09824; S08824.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 GLALCALGGGGPGLRPPP-GC-PQRRLG-ARERRDVQREILAVLGLPGR-PRPRAPPAAS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UL61.
HUMAN CYTOMEGALOVIRUS (STRAIN AD169).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE.
                                                                                                                                                                                                                                                    A MEDILARE, SUCHAGELEBERG P. N. J., JIN D.F., CLIFFORD G.M.,
A WARREN F.D., DRIER E.A., OPPERMANN H.;
J. BIOL. CHEM. 267.2520-25227(1992).
C.-1. FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF EDITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION AND BONE HOMEOSTAS. (SP. SIMILARITY).
C.-1. SUBUNIT: HOWODIMER, DESULFIDE-LIRRED.
C.-1. SUBUNIT: BELONGS TO THE TGF-BETA FAMILY.
REMBL, M97016; G189390; -.
REMBL, M97016; G180390; -.
REMB
                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
BONE MORPHOGENETIC PROTEIN 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 3.32e-03;
12; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
8F20C81B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-A0G-1990 (REL. 15, CREATED)
01-A0G-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROFEIN UIG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 39.7%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263
402
367
401
401
343
343
                                                                                                                                  HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=HIPPOCAMPUS;
MEDLINE; 93094231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
264
301
330
334
366
158
158
402 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 SLP 255
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P16818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 RLP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
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                                                                             ;
                                                                                                             44 LRTYFRDEL-FTMNGRELVPTP-R-AEALAPAVREALLHIHLSIISWDPFNPAQSDRSFR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 93094231.

OEZKAYNAK E., SCHNEGELSBERG P.N.J., JIN D.F., CLIFFORD G.M.,
WARREN F.D., DRIER E.A., OPPERAANN H.;
J. BIOL. CHEM. 267:25220-25227(1992).

-1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE
OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION
AND BONE HOMEOSTASIS (BY SIMILARITY).

-1- SUBUNIT: HOMODIMER, DISOLETIDE-LIRKED.
-1- DEVELOPMENTAL STRACE: EXTENSIVE EXPENSIVE EXPENSIVE
FELL DRASTICALLY IN 10-DAY EMBRYOS AND VIRTUALLY ABSENT IN 17-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BONE MORPHOGENETIC PROTEIN 8A PRECURSOR (BMP-8A) (OSTEOGENIC PROTEIN
                                                                                                                                  12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAY EMBRYOS.

-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

EMBL, M97017, 2200141; -.

MGD: MGI:104515; BMP8.

PROSITE; PS00250; TGF_BETA; 1.

SIGNAL: GROWTH FACTOR: CYTOKINE; BONE; CARTILAGE; GLYCOPROTEIN.
                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                            BMPĜA OR BMP8 OR BMP-8.
MUS MUSCULUS (MOUSE).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
BOTENTIAL.
BOYENGENETIC PROTEIN 8A.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHIN (BY SIMILARITY).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 118; DB 1; Length 399;
Pred. No. 3.30e-02;
12; Mismatches 22; Indels
                                  Length 322;
                                    Score 121; DB 1; Length 322
Pred. No. 1.25e-02;
23; Mismatches 35; Indels
36460 MW; FA5238EE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7075A1ED CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 AA.
                                                                                                                                                                                                                                                                                                  Æ
                                                                                                                                                                                                          : | :::: : |:|: | || || || 95 QVSCLKELVARV-LQRLCERGAKNVLAFGFALL 126
                                                                                                                                                                                   101 -II-LSDFMTLMFLERVVVRVAREAPAVSFELL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.4%;
Best Local Similarity 38.7%;
Matches 24; Conservative
                                                     Best Local Similarity 30.1%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363
155
340
399 AA;
322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-EMBRYO
                                                                                                                                                                                                                                                                             LT 12
BM8A_MOUSE
P34821;
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BMP8_HUMAN
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CARBOHYD
SEQUENCE
SEQUENCE
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                                    Query Match
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PROPEP
CHAIN
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5; Gaps

431 AA

DB 1; Length 402;

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9
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                                                                                                                                                                                                 268 RGGGGKPPLGSPRA-TDGNRDPG-A-GVPARPGRRMGGSSGGRGGTPGRGPERAAPGARP 324
                                                                                                                                                                                                                                   15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST ANOUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANOUATION UPDATE)
MESENCHIME FORK HEAD PROTEIN I (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                    6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 97312712.

MEDLINE; 97312712.

MEDLINE; 97312712.

MIUTAN N. IIDA K., KAKINUMA H., YANG X.-L., SUGIYAMA T.; GENOMICS 41:489-493(1997).

-!- FUNCTION: MIGHT BE INVOLVED IN THE FORMATION OF SPECIAL MESENCHYMAL TISSUES (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).

-!- SIMILARITY: CONTAINS I FORK-HEAD DOMAIN.

R MIM: 602402; ...

R PROSITE; PSO0659; FORK HEAD_1; 1.

R PROSITE; PSO0659; FORK HEAD_2; 1.

R PROSITE; PSO0659; FORK HEAD_2; 1.

R PROSITE; PSO0659; FORK HEAD_2; 1.

PROSITE; PSO0659; FORK HEAD_3; 1.

T DOMAIN 163 167 POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                       Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 125, DB 1; Length 501
Pred. No. 3.32e-03;
28; Mismatches 38; Indels
                                                                Score 118; DB 1; Length 431
Pred. No. 3.30e-02;
20; Mismatches 31; Indels
44309 MW; 232AB9D7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-ALA.
99D32EFA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIS-RICH.
ALA/PRO-RICH.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                               325 TAPDGAPGRWDGPADGPAPGLGRG 348
                                                                                                                                                                                                                                                                                                                                                                           270 RTPVG-QGSWAHPGRTRGPS-DRG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416 422 P
501 AA; 53719 MW;
                                                                Query Match 1.4%;
Best Local Similarity 32.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.4%;
Best Local Similarity 28.4%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FKH-14).
FKHL14 OR MFH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15

ID MEHLLHUMAN
AC 099958;
DT 15-JUL-1998
DE MESENCHIME F
DE FKH-14).
GN HOMO SAPIENS
OC EUTHERIA; PR
RP SEDUENCE FRO
RP SEDUENCE FRO
RN (1]
RA MURA N., II
GENOMICS 41:
CC -!- FUNCTION
CC -!- FUNCT
SQ SEQUENCE
                                                                                                                                                                                                 සු
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Search completed: Thu Dec 24 07:51:35 1998 Job time : 193 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Dec 24 07:51:54 1998; MasPar time 76.57 Seconds 750.503 Million cell updates/sec Run on:

not generated. Tabular output

Title: Description: Perfect Score: Sequence:

1 HASGORCVLLRTWEALAPAT.....TALEAAANPALPSDFKTILD 1154 >US-08-951-733-20 (1-1154) from US08951733.pep 8624

PAM 150 Gap 11 Scoring table:

165420 seqs, 49795644 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptremb16

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_lnvertebrate 6:sp_nammal 7:sp_mhc 8:sp_organelle 9:sp_hage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 54.168; Variance 101.474; scale 0.534 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	0.00e+00	0.00e+00	0.00e+00	1.37e-110	3.12e-111	1.97e-60	2.25e-57	1.71e-35	7.18e-06	2.85e-05	4.02e-05	5.65e-05	3.03e-04	7.93e-05	4.23e-04	3.03e-04	3.01e-03	1.57e-03	3.01e-03	1.14e-03
	Description	TELOMERASE REVERSE TRA	TELOMERASE CATALYTIC S	TELOMERASE REVERSE TRA	TELOMERASE REVERSE TRA		TELOMERASE SUBUNIT P12	TELOMERASE CATALYTIC S	CHROMOSOME XII COSMID	HYPOTHETICAL PROTEIN (WISKOTT-ALDRICH SYNDRO	PAROTID 'O' PROTEIN (F	IS 1222 GENE ORF-A AND	HOMEOBOX PROTEIN (FRAG	POLYKETIDE SYNTHASE (F	HYPOTHETICAL 60.2 KD P	PLENTY - OF - PROLINES - 101	HOMOLOGUE OF RETROVIRA	PROLINE RICH PROTEIN.	SALIVARY PROLINE-RICH	PROLINE RICH PROTEIN P
	OI OI	014746	014783	070372	013339	013338	000939	035432	206163	069118	036027	009000	046612	920660	054226	041935	070495	085301	Q61888	Q04118	062103
	DB	4	4	11	m	m	S	11	٣	14	٣	7	~	4	7	14	11	14	11	4	11
	Query Match Length DB	1132	1132	1122	886	686	1031	67	884	296	574	234	276	316	373	585	897	264	300	309	317
øР	Query	98.2	98.1	59.8	7.9	7.9	5.1	4.9	3.6	1.7	1.7	1.6	1.6	1.6	1.6	1.6	1.6	1.5	1.5	1.5	1.5
	Score	8465	8459	5161	678	681	439	424	314	147	143	142	141	136	140	135	136	129	131	129	132
	Result No.	-	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20

4.15e-03 8.18e-04	2.18e-03	1.27e-01	9.42e-02	1.08e-02	9.42e-02	9.42e-02	9.42e-02	9.42e-02	2.02e-02	1.48e-02	2.02e-02	1.08e-02	9.42e-02	2.76e-02	1.48e-02	2.32e-01	2.32e-01	1.72e-01	2.32e-01	2.32e-01	1.72e-01
BETA-KETOACYL SYNTHASE SIMILARITY TO COLLAGEN 1.F3 PROTEIN	HYPOTHETICAL 131.9 KD	C04G2.8.	CODED FOR BY C. ELEGAN	PROLINE-RICH SALIVARY	SUBSTRATE OF THE PROTE	MPIK3030 NODD1 GENE IN	EXONUCLEASE SBCD HOMOL	FLHF.	CHITINASE PRECURSOR.	EXTENSIN (FRAGMENT).	PRPL-2 PROTEIN.	WASP INTERACTING PROTE	VIRAL PROTEINASE.	SF16 ISOLOG.	SER/ARG-RELATED NUCLEA	HYPOTHETICAL 9.9 KD PR	PROLINE-RICH PROTEIN.	PROLINE-RICH PROTEOGLY	PRBIM PROTEIN (FRAGMEN	CON1.	SEQUENCE OF BAC F20P5
Q53913 002123 099307	006264	017626	P91497	062107	085028	053180	068033	052256	042421	041645	015220	043516	085027	022835	060585	041981	064306	007611	016038	000599	004528
2 2 2	(A) 4																				
	2 4	Ŋ	S	11	14	7	7	7	12	10	4	4	14	10	4	14	11	H	4	4	10
527				227 11	٦	322 2				464 10	4 64 4	503 4	526 14	657 10		Н	-	-	297 4	382 4	488 10
1.5 527		197		227 1	٦		405			1.4 464 10			٠.	1.4 657 10	820	Н	-	295 1	1.3 297 4	1.3 382 4	1.3 488 10
128 1.5 527 133 1.5 539 132 1.5 924	1.5 1236	7 1.4 197	8 1.4 203	5 1.4 227 1	1.4 236 1	1.4	1.4 405	1.4 437	1.4 439	1.4	1.4	1.4	1.4 526	1.4	1.4 820	1.3 106 1	260 1	1.3 295 1	1.3	5 1.3 3	1.3
0.00 edeler	130 1.5 1236	117 1.4 197	118 1.4 203	125 1.4 227 1	118 1.4 236 1	118 1.4	118 1.4 405	2 118 1.4 437	123 1.4 439	124 1.4	123 1.4	1.4	118 1.4 526	122 1.4	124 1.4 820	115 1.3 106 1	115 1.3 260 1	1.3 295 1	115 1.3	115 1.3 3	5 1.3 4

ALIGNMENTS

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11 1 014746 P 014746; 01-7446; 01-7446; 01-744-1998 (01-7	SAPIENS RYOTA; ME	ENCE FROM INE, 9740 INE, 9740 INE, 1, H NCE 27:9 NCE 27:9 NCE 27:9 NCE 27:9	Query Match Best Local Simil Matches 1132;		DARPPAA DARPPPAA	SYLPNTVI 		-
RESULT 1 ID 014746 AC 014746; DT 01-JAN- DT 01-JAN- DT 01-JUN- DT 11-JUN-	HIRI. HOMO S EUKAR EUTHEI	SEQUENCE TISSUE-KI MEDLINE; MAKAMURA LINGNER J SCIENCE Z EMBL; AFG RNA-DIREC SEQUENCE	Query Match Best Local Matches 11	73	61	121	181	241
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EUTHERIA; PRIMATES.
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MEYERSON M., COUNTER C.M., EATON E.N., EL CADDLE S.D., ZIAUGRA L., BELJERSBERGEN R. BACCHETTI S., HABER D.A., WEINBERG R.A.; CELL 90:788-795(1997).
EMBL, AF018167; G2347129; -.
SEQUENCE 1132 AA; 126937 MW; CLE5EZAF
                                                             Query Match 98.1%;
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612 RQHLKRVQLRELSEAEVRQHREARPALLISRLRFIPKPDGLRPIVNMDYVVGARTFRREK
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SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF015783; G2340168; -.
EMBL; AL022299; E1285360; -.
EMBL; PAPA: PF00078; FY EN EMBL; PAPA: PR00078; FY EN EMBL; PAPA: PR00078; FY EN EMBL; PAPA: PR00078; FY EN EMBL; PAPA: PA
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
TELOMERASE REVERSE TRANSCRIPTASE 1.
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MADLINE; 97400623.
MAKAWUR T.M., MORIN G.B., CHAPMAN K.B., WEINRICH LINGNER J., HARLEY C.B., CECH T.R.;
SCIENCE 277:955-959(1997).
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
TELOMERASE REVERSE TRANSCRIPTASE.
MUS MUSCULLOS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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GREENBERG R.A., ALLSOPP R.C., CHIN L., MORIN G.B
ONCGENB 0:0-0(1998).
EMBL. AF051911; G3005592; -.
RNA-DIRECTED DNA POLYMERASE.
SEQUENCE 1122 AA; 127977 WW; 222075D6 CRC32;
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MEDLINE; 97400623.
NAKAMURA T.M., MORIN G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H.,
LINGRER J., HARLEY C.B., CECH T.R.;
SCIENCE 277:955-959(1997).
EMBL; AF015783; G2340169; -.
PFAM; PF00078; rvt.
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In 7.9%; Score 678; DB 3; Length 988; Similarity 26.4%; Pred. No. 1.37e-110; L29; Conservative 133; Mismatches 208; Indels 18;
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1 Similarity 26.3%; Pred. No. 3.12e-111;
129; Conservative 136; Mismatches 204; Indels
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
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989 AA; 116456 MW; FDE74202 CRC32;
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                                                                                                                                                                                    |: :: : | : : : : : : : | NM-D-YVVGARTERREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRT
                                                                                                                                                                                                                                                                                                                                                                                           LSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVLLRVVDDFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478 VIMKMSI-ADLKKETLAEVQEKEV-EEWKKSLGFAPGKLRLIPKKTTFRPI--MTF--NK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  605 KLOSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGA
                                                  458 YFRKDIW-KLLCRPFITSMKMEAFEKINENNVRMDTQ-KTTLPPAVIRLLPKKNTFRLIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 5.1%; Score 439; DB 5; Length 1031;
Local Similarity 23.0%; Pred. No. 1.97e-60;
les 142; Conservative 168; Mismatches 261; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 97274210.
LINGNER J., HUGHES T.R., SHEVCHENKO A., MANN M., LUNDBLAD V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JÜL-1997 (TREMBLREL. 04, CREATED)
01-JÜL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
TELOMERASE SUBUNIT P123.
EUPLOTES AEDICULATUS.
EURARYOTAE; MITOCHONDRIAL EUKARYOTES; ALVEOLATA; CILIOPHORA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCIENCE 276:561-567(1997).
EMBL; U95964; G2072336; -.
SEQUENCE 1031 AA; 122562 MW; 21A885CD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1031 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     805 GFSVNMRSLD 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |: :: |:|:
954 GLLLDTRTLE 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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BENES V., BRUCKNER M., DELIUS H., DUBOIS E., DUSTERHOFT A.,
ENTIAN K.D., FLOETH M., GOFFEAU A., HEBLING U., HEUMANN K.,
HEUGS-NEITZEL D., HILBERT H., HILGER F., KLEINE K., KOTTER P.,
LOUIS E.J., MESSENGUY F., MEMES H.W., MIOSGA T., MOSTL D.,
MULLER-AGER S., NENTWICH U., OBERMAIER B., PIRAVANDI E., POHL T.M.,
PORTETELLE D., PURNELLE B., RECHMANN S., RIEGER M., RINKE M., ROSE M.,
SCHARFE M., SCHERENS B., SCHOLLER P., SCHWAGER C., SCHWARZ S.,
UNDERMOD A.P., URRESTARALU L.A., VANDENBOL M., VERHASSELT P.,
WEDLER H., ZIMMERMANN F.K., ZOLLNER A., HANI J., HOHEISEL J.D.;
NATURE 387:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 LSHLSRQSPKER-VLKFIIVILQKLLPQEMFGSKKNKGKIIKNLNLLLSLPLNGYLPFDS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 LLKKLRLKDFRWLFIS-DIWFTKHNFENLNQLAIC-FISWLFRQLIPKIIQTFFYCTEIS 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 KSNNEFRIIAIPCRGADEEEFTIYKENHK-NA-IQPTQKILEYLRNKRPTSF-TKIYSPT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       659 PSQDTLILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKAN-RDKILAVSSQSDDDTV 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 QIADRI-KEFKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMR-ILKDALKNENGFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      559 VRSQY-FFNTNT-G-VLKLFNV-VNASRVPKPY-ELYIDNVR-TVHLSNQDVIN---VV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E----M-EIF-K-T---ALWVEDKCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            822 EASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDM-E-NKLF-AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 STVIIVYF-RHDTWNKLITPFIVEYFKTY-LVE-NNV-CRNHNSYILSNFNHSKMRIIPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 3.6%; Score 314; DB 3; Length 884; Best Local Similarity 24.3%; Pred. No. 1.71e-35; Matches 118; Conservative 122; Mismatches 202; Indels 44;
                                                                                                                                                                                                                                                                                SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                     WATERSTON R.;
SUBMITTED (FEB-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             884 AA; 102662 MW; 1A94320F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., STRAIN-S288C (AB972); CHERRY J.M.; SUBMITIED (JUL-1997) TO EMBL; UZ0618; G662136;
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    718 IQFCAM 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    939 TAFVQM 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Q69118
Q69118;
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ID Q6
AC Q6
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STRAIN-S288C (AB972);
MEDLINE; 97313267.
JOHNSTON M., HILLIER L., RILES L., ALBERMANN K., ANDRE B., ANSORGE W.,
                                                                                                                                                                                                                                                                                                                                     888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            711 QPVIN-ICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPE 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                      651 FRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKTLIVEAKQRNYFKKDNLL
                                                                                                                         770 NPNVNLLMRLTDDYLLITTQENNAVLFIEKLINVSRENGFKFNMKKLQTSFPLSPSKFAK
                                                                                                                                                                                                                                                                KKLKSFL-MNNITHYFRKTITTEDFANKTLNKLFISGGYKYMQCAKE--YKDHFKKNLAM
                                                                                                                                                                                         YGMDSVEEQNIVQDYCDWIGISIDMKTLALMPNIN-LRIEGILCTLNLNMQTKKASMWLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
TELOMERASE CATALYTIC SUBUNIT (FRAGMENT).
MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 2.25e-57;
10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18543.12.
SACCIAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRISSI R., CLEVELAND J.L.;
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA
EMBL; AF029235; G2605903; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E2A06F2B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            884 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER 1 1
NON_TER 67 67
SEQUENCE 67 AA; 8368 MW;
                                                                                                                                                                                                                                                                                                                                                                                                    1054 FLRVISDTASLCYSILKA 1071
                                                                                                                                                                                                                                                                                                                                                                                  946 SSMIDLEVSKIIYSVTRA 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL. 01,
01-AUG-1998 (TREMBLREL. 07,
CHROMOSOME XII COSMID 8543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 4.9%;
Best Local Similarity 76.1%;
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLRFIPK 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RLRFIPK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LT 8
Q06163
Q06163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 7
035432
035432;
                                                                                                                                      829
                                                                                                                                                                                                                                            830
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Gaps

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321 VGRQHHAGPPSTSRPPRPWDTPCPPV 346

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 SAPPPPPRSAPSTGRQPPPLSSSRAVSNPP--APPPAIPGRSAPALPPLGNASRTSTPP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 AANKKRPPPPPP-PSRR---NRG-KPPIGNGSSNSSLPPPPPPPPRSNAAG-SIPLPPQGR 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 143; DB 3; Length 574;
Pred. No. 2.85e-05;
41; Mismatches 53; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 147; DB 14; Length 296;
Pred. No. 7.18e-06; .
20; Mismatches 33; Indels
                                                                                                                                                                                                                                                            PFITZNER A.J., TSAI E.C., STROMINGER J.L., SPECK S.H.; J. YROL. 61:2902-2909(1987).
EMBL: MIY294; G80766; --
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=JS21;
ZANKEL T.C., OW D.W.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . -> V (IN STRAIN JS21).
9E84D37C CRC32;
  01, CREATED)
01, LAST SEQUENCE UPDATE)
01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               036027;
01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG 1.
WSP1 OR SPAC4F10.15C.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 IGGRPAAPGAPGTPAAPGPGGGAAVPSGATPHPERGSGPAD 187
                                                                                                                              VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE;
GAMMAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                            296 AA; 31393 MW; D17CEF6F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-PRO.
POLY-PRO.
POLY-PRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                             HYPOTHETICAL PROTEIN (FRAGMENT).
HUMAN HERPESVIRUS TYPE 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.7%;
Best Local Similarity 28.8%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 38.6%;
Matches 39; Conservative
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343
366
248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 3
248 2
574 AA;
                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 87284169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                    NON_TER
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LT 12
046612;
046612;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLEL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLEL. 06, LAST ANNOTATION UPDATE)
1S 1222 GENE ORF-A AND ORF-B.
BYNTENDANCTER AGGLOMERANS.
PROMERRYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 RPRRGAAPEPERTPVGQGSWAHPGRTRGPSDR-GFCVVSPARPAE-EATSLEGALSGTRH 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 QGGNQSQG-PPPHPGKPERPPP-QGG-NQSHRPPPPP-GKPER-PPPQGGNQSQG-P-PP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 HPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPGGNPQQPQ 204
                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZEN E.A., AMBERGER E., FISHER S., PRAKOBPHOL A., NIECE R.L.;
AM. J. HUM. GENET. 58:143-153(1996).
EMBL; S80916; G1911492; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.6%; Score 142; DB 4; Length 234 Best Local Similarity 28.2%; Pred. No. 4.02e-05; Matches 40; Conservative 41; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STEIBL H.D., SIDDAVATTAM D.;
SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                              04, CREATED)
04, LAST SEQUENCE UPDATE)
04, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0B54A420 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 234 AA; 23656 MW; B5920075 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
96422789 94427878
STEIBL H.D., SIDDAVATTAM D., KLINGMUELLER
PLASMID 34:223-228(1995).
                                     234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STEIBL H.D.;
THESIS (1995), UNIVERSITAET BAYREUTH.
EMBL; X78052; G459248; -.
EMBL; X81893; E258949; -.
                                     PRT;
                                                                                                                            (TREMBLREL. 04, LAST (TREMBLREL. 04, LAST PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 APPAGKPQGPPPPPQGGRPPRP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 AA; 31718 MW;
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STRAIN=KLEEBERGER, 1983;
MEDLINE; 9525564.
STEIBL H.D., LEWECKE F.M.;
GENE 156:37-42(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : |: | : || :||||| 317 SHPSVGRQHHAGPPSTSRPPRP
                                     PRELIMINARY;
                                                                                                     (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 96108975.
                                                                                              01-JUL-1997
01-JUL-1997
01-JUL-1997
PAROTID '0'
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LT 11
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                                                                                                                                                                                :|| :::: | | || :: | | : || : || 585 VIETIFQKNRLFFYRKSVWSKLQSIGIRQHLKRV-QLRELSEAEVRQHREARPALLISRL 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 RPWSTASSDCSVGRTGIAPRGPAT-SPRPSRSPAAQDRSRPARSAPGPAASPGGPGAWTH 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 ITELALERRR-FGYRR-IWQLLRREGLHVNHKRVYRLYHLSGLGVKRRRR-RKGLATERL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HB9.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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STRAIN-NRRL2338.
SALAH-BEY K., DOUMITH M., MICHEL J.M., HAYDOCK S., CORTES J.,
LEADLAY P.F., RAYNAL M.C.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, 114332; E1228185; -.
SEQUENCE 373 AA; 40872 MW; 781BECGD CRC32;
          Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 1.6%; Score 136; DB 4; Length 316; Best Local Similarity 30.9%; Pred. No. 3.03e-04; Matches 21; Conservative 20; Mismatches 24; Indels
Score 141; DB 2; Length 276
Pred. No. 5.65e-05;
23; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SACCHAROPOLYSPORA ERYTHRAEA (STREPTOMYCES ERYTHRAEUS)
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; NOCARDIOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      054226;
01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
POLYKETIDE SYNTHASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 129 HOMEOBOX.
112 121 H-T-H MOTIF.
316 AA; 34713 MW; 1531E766 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ź
                                                                                                                                                                                                                                                                                99 PLL-RPAAPNLTWSDDFVMDALATGRRIK 126
                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
       Query Match 1.6%;
Best Local Similarity 33.7%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOMEOBOX PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-TONSIL;
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DNA_BIND
DNA_BIND
SEQUENCE
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Q99076
Q99076;
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Gaps 11;
                                    Gaps 11;
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VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE; GAMMAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 PPP-ELGPGSPTSPAPSRAGARIPDLPGPLPSWGPDPRPPRPPPELGPGSPTSPAPSRAG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 ARIPDLPGPLPSWGPDPRPPRPPPELGP-GSPT-SPAPSRAGARIPRPSRPPPELGP--G 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 PRRRAA-NRRRG-AAPAPGIAPG-AAHG-HRRG-AARRARDRRRRGGRGRRRGGOPRPGG 297
                                                                                                                      298 L-RRARPPR-RGPPRRRPRAVGTSRPPRQAGG-AGH-R-ARHRRTA-GRGQGAARTHAQR 351
                                                                                                                                                                                                                 275 QGSWAHPGRIRGPSDRGFCVVSPARPAEEAISLEGALSGIRHSHPSVGRQHHAGPPSISR 334
Score 140; DB 2; Length 373;
Pred. No. 7.93e-05;
27; Mismatches 46; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-WUMS;
MEDLINES, 973-66649.
WINGIN H.W. IV, LATREILLE P., WAMSLEY P., HALLSWORTH K., WECK
DAL CANTO A.J., SPECK S.H.;
J. VIROL. 71:5894-5904(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 135; DB 14; Length 585;
Pred. No. 4.23e-04;
37; Mismatches 68; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STARIN-WUMS;
LATREILLE P., WAMSLEY P., WATERSTON R.H.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U97553; G2317934; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 585 AA; 60160 MW; B35C72E5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 ALSGTRHSHPSVGROHHAGPPSTSRPPRPMDTPCPPVYAETKH 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPREPRPSRPP--PELGPGSPDLPGPLPSWG-PDPPTFPAPSR 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
HYPOTHETICAL 60.2 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                585 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
Query Match
Best Local Similarity 32.3%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.6%;
Local Similarity 27.6%;
les 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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protein - protein database search, using Smith-Waterman algorithm

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514.262 Million cell updates/sec Thu Dec 24 07:36:48 1998; MasPar time 36.31 Seconds Run on:

not generated. Tabular output

>US-08-951-733-20 (1-1154) from US08951733.pep 8624

Description: Perfect Score:

1 HASGQRCVLLRTWEALAPAT.......1ALEAAANPALPSDFKTILD 1154 Sequence:

Scoring table:

131922 seqs, 16180660 residues Searched:

summaries Minimum Match 0% Listing first 45 Post-processing:

a-geneseq32
lipart1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
24:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 Database:

Mean 39.946; Variance 185.025; scale 0.216 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CTUNANTE

					SUMMARIES		
		æ					
Result		Query					
No.	Score	Match	Match Length DB	DB.	ID	Description	Pred. No.
1	134	1.6	509	٦,	P91060	Predicted amino acid	3.67e-01
7	117	1.4	386	22	W18664	Fragmented human NF-H	5.36e+00
m	118	1.4	399	-	R23846	Prepro form of human	4.60e+00
4	118	1.4	399	53	W40193	Mouse OP-2 protein.	4.60e+00
Ŋ	118	1.4	399	53	W44314	Mouse osteogenic prot	4.60e+00
9	118	1.4	399	16	R85759	mOP-2.	4.60e+00
7	118	1.4	399	10	R54938	Osteogenic protein mO	4.60e+00
ω	118	1.4	399	7	R33908	Mouse osteogenic prot	4.60e+00
0	118	1.4	399	σ	R46744	Mouse osteogenic prot	4.60e+00
10	118	1.4	399	10	R50201	Murine OP-2.	4.60e+00
11	118	1.4	399	σ	R47253	mOP2.	4.60e+00
12	118	1.4	399	13	W00239	Mouse osteogenic prot	4.60e+00
13	118	1.4	399	56	W36856	Full length sequence	4.60e+00
14	118	1.4	399	10	R57974	Murine OP-2.	4.60e+00
15	118	1.4	399	^	R33411	Murine pro-OP-2-PP.	4.60e+00
. 16	118	1.4	399	12	R51646	mOP2-PP prepro form m	4.60e+00
17	118	1.4	399	25	W23144	Bone morphogenic prot	4.60e+00
18	118	1.4	399	σ	R47293	щОР2.	4.60e+00

4.60e+00	4.60e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.54e+00	1.80e+00	2.11e+00	9.89e+00	8.49e+00		8.49e+00	8.49e+00
Murine osteogenic pro	Murine OP-2.	Human OP-2 protein.	Full length sequence	Human osteogenic prot	Osteogenic protein OP	Osteogenic protein ho	Human osteogenic prot	1	hop2.	Human osteogenic prot	OP-2-PP.	Human osteogenic prot		£	Human OP-2.	Human OP-2.	hop-2.	Human OP-2.	Human hippocampal ost		Sugar beet chitinase		Sequence encoded by n	Morphogen hOP2 full l	Mycobacterium tubercu	Mycobacterium tubercu
R27292	R50239	W40192	W36855	W44315	R60578	R54937	R27291	R47292	R47252	R44759	R33410	W00238	R46732	R51647	R57973	R50238	R85760	R50200	W16366	R33907	R28150	P60623	P70350	R33933	W31855	W31852
'n	10	53	56	29	I	10	Ŋ	σ	σ	œ	7	19	σ	17	10	10	16	10	23	7	S	m	7	^	28	28
399	399	402	402	402	402	402	402	402	402	402	402	402	402	402	402	402	402	402	402	402	439	183	321	402	572	763
1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.3	1.3	1.3	1.3	1.3
118	118	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	124	123	113	114	114	114	114
19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

PER 24-MAY 1989.

24-MAY 1988; 118266.

PF 02-NOV-1988; 03-10536-M.

PR 03-NOV-1988; 03-10516.

PA (ARVU) Baylor Collage Med (NOVA-).

RIANU) Baylor Collage Med (NOVA-).

RIANU) Baylor Collage Med (NOVA-).

PI (ARVU) Baylor Collage Med (NOVA-).

PT (AR Predicted amino acid sequec of the infectious bovine rhinotracheitis virus (IBRV) gill polypeptide
Infectious bovine rhinotracheitis virus; IBRV; gill gene;
gill polypeptide; glycoprotein III; Bovine Herpesvirus type 1;
IBRV(NG)dltkdlgIII; IBR disease vaccine;
Infectious bovine rhinotracheitis disease vaccine.
Infectious bovine rhinotracheitis virus (IBRV)/Bovine Herpesvirus type 1
BP-316658-A. Query Match
1.6%; Score 134; DB 1; Length 509;
Best Local Similarity 29.5%; Pred. No. 3.67e-01;
Matches 31; Conservative 28; Mismatches 41; Indels P91060 standard; protein; 509 AA. P91060; 12-APR-1990 (first entry) RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prods. for the diagnosis, prevention and treatment of associated diseases, e.g. cancer or neuro:degenerative disease.

Claim 22; Fig 9; 123pp; English.

Wi8663 and Wi8664 are +2 and +1 frameshift mutations, respectively, of a sequence comprising fragments of the coding sequence of the human neurofilament subunit NF-H gene corresponding to nucleotides.

Claim 1162 of the Wild-type NF-H gene. This region contains GACAG motifs.

Frameshift mutants of the tau, ubiquitin, apolioporotein E, microtubule-associated protein 2 (MPP-2), neurofilament subunit L, M and amyloid A4 genes are claimed. All these genes share a common CG dinucleotide deletion(s) that cause neurodegenerative disorders.

Chigenic peptides used for the production of antibodies, and small neurolectic acid sequences derived from frameshift mutants are used in the
                                                                                                                                             Fragmented human NF-H gene +1 frameshift mutant product.
Fragmented human NF-H gene +1 frameshift mutantion; diagnosis;
Frameshift mutation product; GAGA motif; somatic mutation; diagnosis;
detection; antibody; probe; cancer; neoplasia; neurodegenerative;
Parkinson's; Alzheimer's disease; Pick's; Huntington's disease;
Down's syndrome; frontal lobe dementia; progressive supranuclear palsy;
PSP; amyotrophic lateral sclerosis; multiple sclerosis; MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases, e.g. Parkinson's disease, Alzheimer's disease, Down's syndrome, frontal lobe dementia (Pick's disease), progressive supranuclear palsy (PSP), amyotrophic lateral sclerosis, Huntington's disease, multiple sclerosis, and other degenerative diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aggplry-gravrargprdarrgaapgrgarsatpgagaparghrarapaprrrgpaarg 286
239 PAPGARRRGGSASRS-LPLPKRPR-RGAAPEPERTPVGQGSWAHPGRTRGPSD-RGFCVV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 AGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis, prevention and treatment of cancer and neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of mutant genes having frame:shift mutation(s) - for developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                            /note= "X corresponds to a stop codon in the accompanying DNA file, T69796"
                                                                                                                                                                                                                                                                                                                                                           /note= "antigenic peptide used fro antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 FCVVSPARPAEEAISLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          grgggpragalraggrggargpaeegagagaggvrlpaapppgrggra 333
                             tpppappedgrpggagnasrdgrpsgggrprpprpskappkerkw 140
                                              Score 117; DB 22; I
Pred. No. 5.36e+00;
26; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiovascular disease and rheumatoid arthritis.
Sequence 386 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grosveld FG, Van Leeuwen FW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 02-0CT-1995; GB-020080.
11-JAN-1996; US-009832.
(ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
                                                                                                                                                                                                                                                        cardiovascular; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                    Location/Qualifiers
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W18664 standard; Protein; 386 AA.
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Matches 30; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burbach JPH, Grosv
WPI; 97-226235/20.
N-PSDB; T69796.
                                                                                                                                                                                                                                                                                                  misc difference
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New osteogenic polypeptide(s) and their dimeric proteins - useful in association with a matrix for bone reconstitution after orthopaedic and plastic surgery.

Disclosure; 51-53; 69pp; English.

The sequence encodes the prepro form of human osteogenic polypeptide-2 (hOP2-Pp). The protein is useful as a subunit of osteogenic proteins capable of endochondral bone formation, and allogenic and xenogenic implants in mammals. When implanted with a matrix, the polypeptide locally induces the full developmental cascade of endochondral bone formation on marrow differentiation. This can be used for optimal predictable bone formation to correct, egacquired or congenital cranofacial and other skeletal or dental anomalies, and to treat non-union fractures. The polypeptide also have dental and periodochial appliens, and may be used for cartilage
                                                                                                                                                              dental abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :| ||:: :|||| : |:|||| | ::|
194 GPPLYQLGAATQA-RPPPHASGPRRRIGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 glalcalggggggglrppp-gc-pqrrlg-ardrdvg-reilavlglpgr-prprappaas 66
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Mouse OP-2 protein.
Osteogenic protein; OP-2; bone morphogenic protein; OP/BMP family; chronic renal failure; renal therapeutic agent; disease; diabetes;
                                                                                                                                                                                                                                                                                            13..18
'label* cleavage site for signal peptide removal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                 form mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repair, eg in osteoarthritis treatment. See also W09105802. Sequence 399 AA;
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/label= conserved seven cysteine skeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 118; DB 1; Length 399
Pred. No. 4.60e+00;
13; Mismatches 19; Indels
                                                                                                                                       prepro sequence; implant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved six cysteine skeleton
                                                                                 05-NOV-1992 (first entry)
Prepro form of human osteogenic polypeptide-2.
Human osteogenic polypeptide-2; prepro sequence; impleendochondral bone formation; skeletal abnormality; der non-union fracture; cartilage repair; osteoarthritis; periodontal applicn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CREA-) CREATIVE BIOMOLECULES INC.
Kuberasampath T, Oppermann H, Ozkaynak E, Rueger DC;
WPI; 92-167153/20.
N-PSDB; N24522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               truncated protein 'hOP2-P'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= truncated protein \hOP2-R'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     truncated protein 'hOP2-S'
                                                                                                                                                                                                                                                                                                                                                                                                               /label= mature protein \hOP2-A'
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                                                                                                                                                                                                                                                                                                                                                                 cleavage site
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л.
R23846 standard; Protein; 399 АА.
R23846;
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Best Local Similarity 39.7%;
Matches 25; Conservative
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240.399
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267..399
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                                                                                                                                                                                                                                        Homo sapiens.
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18-OCT-1991;
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ID W4
AC W4
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Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treatment of chronic renal failure - using an osteogenic

Protein/Pone morphogenetic protein renal therapeutic agent or

Protein/Pone morphogenetic protein renal therapeutic agent or

morphogen or renal mesenchymal progenitor cells

This sequence represents the mouse osteogenic protein, OP-2. This

This sequence represents the mouse osteogenic protein, OP-2. This

Crisk of, chronic renal failure which comprises administering an

osteogenic protein/Done morphogenetic protein (OP/BMP) renal having, or at

crisk of, chronic renal failure which comprises administering an

osteogenic protein/Done morphogenetic protein (OP/BMP) renal therapeutic

agent or morphogen. The method can be used for treating e.g. chronic

agent or morphogen. The method can be used for treating e.g. chronic

clanal failures, end'stage renal disease, chronic diabetic apphropathy,

diabetic glomerulopathy, diabetic renal hypertrophy, hypertuphy,

administerion hypertrophy, tubular hypertrophy,

clinicated with e.g. glomerular hypertrophy, tubular hypertrophy,

clinicated with e.g. glomerular hypertrophy,

clinication agents can prevent, inhibit or delay the progressive loss of

functional nephron units and the progressive decline in glomerular

clinication rate (GFR) which slowly but inevitably leads to the need for

consistence.
nephropathy; glomerulopathy; hypertrophy; sclerosis; nephritis; mouse; dysplasia; fibrosis; glomerular filtration rate; GFR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches 22; Indels 4; Gaps
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Mouse osteogenic protein OP2.
Mouse; osteogenic protein; subunit; endochondral bone formation;
dimeric; recombinant protein.
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Pred. No. 4.60e+00;
                                                                                                                                                                               18..263
/label= propeptide
264..402
/label= 0p-2
                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              06-MAY-1997; U07816.
06-MAY-1996; US-643321.
(CREA-) CREATIVE BIOMOLECULES INC.
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                                                                                                                         1..17
/label= signal
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Best Local Similarity 38.7%;
Matches 24; Conservative
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US-179406.
US-232630.
US-315342.
US-422613.
US-42269.
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US-579865.
US-599543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cohen CM, Sampath KT;
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23-MAY-1995; 4
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15-AUG-1988;
23-FEB-1989;
17-OCT-1989;
17-CT-1989;
22-FEB-1990;
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07-SEP-1990;
18-OCT-1990;
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The present sequence represents the present invention describes methods used in the present invention. The present invention describes methods used in the present invention. The present invention describes methods for selectively extracting an osteogenic protein (OP) from a mixture. The method comprises: (a) exposing the mixture to an antibody that specifically binds OP, separating the resulting antibody-protein complex from the mixture, and dissociating the complex. In the methods OP comprises a pair of oxidised subunits that are disulphide-bonded to form a dimer, and one of the subunits has an amino acid (aa) sequence sufficiently homologous to residues 335-431 of a 431 aa protein designated OPS, sequence given in the specification. In dimeric form OP is capable of inducing cartilage and endochondral bone formation in a mammal when disposed within a matrix implanted in the mammal. The methods are used for recovering the recombinant proteins from cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Extraction of osteogenic protein from mixture - using antibodies specific for novel polypeptide chains useful as subunit(s) of dimeric osteogenic protein(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 118; DB 29; Length 399;
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12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                 Kuberasampath T, Oppermann H, Ozkaynak E, Pang RHL,
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261..399
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R85759 standard; Protein; 399 AA.
R85759;
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Local Similarity 38.7%;
les 24; Conservative
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17..260
21-NOV-1990; US-616374.
04-DEC-1990; US-621849.
04-DEC-1990; US-621849.
22-FEB-1991; US-660162.
20-DEC-1991; US-810560.
28-JAN-1992; US-810560.
23-MAY-1995; US-447570.
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21-NOV-1995.
08-APR-1988; 179406.
08-APR-1988; US-179406.
15-AUG-1988; US-232630.
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                                                                                                                                                                                                                                                                   (STYC ) STRYKER CORP.
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N-PSDB; V15217.
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28-AUG-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        induce local endochrondral bone formation in non-union fractures and in other clinical applications including dental and periodontal applications where bone formation is required. Other potential applications include cartilage repair, e.g. in the treatment of osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies with osteogenic protein binding specificity - used in purification of osteogenic proteins, and as antigenic proteins bulsclosure; column 139-42; 129pp; English.

This sequence represents the murine osteogenic protein, mOP-2. mOP-2 has homology with proteins in the TGF-beta superfamily. Fragments of the mOP-2 protein can be used in the production of dimeric peptides which may be used in the generation of antibodies with binding specificities for osteogenic proteins. The antibodies are and may be used in purification protocols. Osteogenic protein and may be used in minibulable osteogenic device which allows predictable bone formation to correct acquired and congenital cannot other skeletal or dental anomalias. They may be used to carnofacial and other skeletal or dental anomalias. They may be used to carnofacial and other skeletal or dental anomalias.
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Disclosure; Page 134-136; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 118; DB 16; Length 399;
Pred. No. 4.60e+00;
12; Mismatches 22; Indels
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15-OCT-1994 (first entry)
Osteogenic protein mOP2-PP.
Morphogenic protein; mOP-2-PP; OP-2; mOP2; mOP-2;
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04-MAR-1993; US-029335.
31-MAR-1993; US-040510.
(CREA-) CREATIVE BIOMOLECULES INC.
Cohen CM, Kuberasampath T, Opper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.4%;
Best Local Similarity 38.7%;
Matches 24; Conservative
                                                                                                     US-483913
US-569920
US-599865
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                                                                                                                                                                               07-SEP-1990; UR-0CT-1990; UR-0CT-1990; UR-0CT-1990; UR-0CT-1990; UR-DEC-1990; UR-0CT-1991; UR-0C
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21-FEB-1992;
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                                                                                                         22-FEB-19
20-AUG-19
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The first properties of morphogenic-stimulating agent - to prevent bone loss or increase, used for treating bone fractures, post-menopausal or senile osteoporosis, hyperparathyroidism etc.

Disclosure; Page 122-123; 162pp; English.

The sequence is that of mouse osteogenic protein 2 (mOP-2) a morphogenically active protein which may be used as part of a morphogenically active protein which may be used as part of a morphogenically active protein which may be used as part of a morphogenically active protein which may be used so part of a morphogenically active protein which may be used so part of a morphogenically active protein which are been affected in skeletal reconstructure. Such diseases include chronic renal failure and other kidney diseases, osteomalacia, vitamin D deficiency-induced other kidney diseases, osteomalacia, vitamin D deficiency-induced other kidney diseases, osteomalacia, vitamin D deficiency-induced osteopenia or osteoporosis, postmenopausal females, aged individuals and individuals undergoing postmenopausal females, aged individuals and individuals undergoing dialysis. The loss of bone mass may result from an imbalance in bone resorption or bone formation, an imbalance of calcium or hormonally metabolism, a vitamin D imbalance or be nutritionally or hormonally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence given in 10. cDNA and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 glalcalggghgprpp-htc-pqrrlg-arerrdmqreilavlglpgr-prpragpaaar 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteoporosis, hyperparathyroidism; skeletal microstructure defects; chronic renal failure; kidney disease; osteomalacia, vitamin D; deficiency-induced osteopenia, osteoporosis; paget's disease; bone mass; imbalance; resorption; formation; dialysis; calcium; Mus musculus.
A novel mouse morphogenic protein, OP3, has the sequence given in R54934, and is encoded by CDNA of sequence 065390. CDNA and protein sequences were also provided for human osteogenic protein OP1 (065391, R54935), mouse OP1 (065392, R54936), human OP2 (065393, R54937) and mouse OP2 (065394, R54938), as well as the genomic DNA sequence of human OP2 (065395). Generic sequences given in R54939-40 accommodate homologies between OP1, OP2, OP3 and other morphogen Sequence 399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Score 118; DB 10; Length 399; Pred. No. 4.60e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "conserved seven cysteine skeleton"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R33908;
21-JUL-1993 (first entry)
Mouse osteogenic protein 2 (mOP-2).
Bone; loss; increase; fracture; post-menopausal; senile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cohen CM, Kuberasampath T, Oppermann H, Ozkaynak E,
Pang RHL, Rueger DC, Smart JE;
WPI; 93-117208/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "mature protein"
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30-AUG-1991; US-752857.
30-AUG-1991; US-752861.
31-UUL-1992; US-923780.
(CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R33908 standard; Protein; 399 AA.
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Local Similarity 38.7%;
les 24; Conservative
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/note= "n
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17-FEB-1994.
29-JUL-1993; U07189
                            31-MAR-1994.
15-SEP-1993; U08885
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N-PSDB; Q56201.
                                                                                                                     N-PSDB; Q45119
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                                                          glalcalggghgprpp-htc-pgrrlg-arerrdmgreilaviglpgr-prpragpaaar 67
                                               glalcalggghgprpp-htc-pgrrlg-arerrdmgreilavlglpgr-prpragpaaar 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                            capable of enhancing tissue morphogenesis, development and viability, e.g. in infants, aged individuals and metabolic disorders, e.g. anorexia nervosa, etc. Disclosure and Claims 25-26; Page 127-129; 160pp; English. Murine osteogenic protein mOP2 and proteins having at least 70% homology with it are preferred morphogens for inclusion in new morphogen-enriched nutritional formulations. The formulations are dietary compositions suitable for people at risk for tissue damage due to protein energy malnutrition or to altered metabolism an infant or juvenile.
                                                                                                                                                                                                     tissue development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4:
                            4;
                                                                                                                                                                                                                                                                                                                                                                    Morphogen enriched dietary compositions and infant formula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 399;
        Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OP-1: OP-2; CBMP2; Vgl(fx); Vgr(fx); DPP(fx); GDF-1(fx); 60A(fx); BMP3(fx); BMP5(fx); BMP5(fx); BMP6(fx); Osteogenic protein; morphogen; morphogen; protein; gastrointestinal tract; luminal lining; epithelial cell; proliferation; ulcer; lesion; inflammation; regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 118; DB 9; Length 399
Pred. No. 4.60e+00;
12; Mismatches 22; Indels
                            Indels
                                                                                                                                                                     25-Aug-1994 (first entry)
Mouse osteogenic protein mOP2.
mouse osteogenic protein; mOP2; murine; morphogen;
infant food formulation; tissue morphogenesis; tissu
bone growth; morphogen-enriched nutritional product.
                                                                                                                                                                                                                                                                                                                              Ozkaynak
                            22;
                 4.60e+00;
        DB 7;
                           12; Mismatches
                                                                                                                                                                                                                                                                                                                (CREA.) CREATIVE BIOMOLECCULS .....
Jones WK, Kuberasampath T, Oppermann Rueger DC, Tucker RF, Cohen CM, Pang
        Score 118;
Pred. No. 4
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R50201;
                                                                                                                                                  R46744 standard; Protein; 399 AA
        1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 1.4%;
Local Similarity 38.7%;
hes 24; Conservative
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      Query Match
Best Local Similarity 38.7%;
Matches 24; Conservative
                                                                                                                                                                                                                                                               31-JUL-1992; US-923780.
31-JUL-1992; US-922813.
16-SEP-1992; US-946235.
04-MAR-1993; US-029335.
31-MAR-1993; US-040510.
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Best Local
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effects of cancer therapy.

Claim 35-36; Page 115-117; 151pp; English.

Norphogens comprising an amino acid sequence sharing at least 70% homology with OP-1, OP-2, CBME2, BMP3(fx), Vg1(fx), Vgr(fx), DPP(fx), GDF-1(fx), 60A(fx) and at least 80% homology with BMP5(fx) are useful for maintaining the integrity of the gastrointestinal tract luminal lining in a mammal, including (1) limiting epithelial cell proliferation, (2) inhibiting ulcerative lesion formation, (3) inhibiting inflammation normally associated ulcerative diseases, and/or (4) stimulating the repair of sequence 399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glalcalggghgprpp-htc-pqrrlg-arerrdmgreilavlglpgr-prpragpaaar 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morphogenic protein soluble complex - for regeneration of tissue in mammals and diagnosing tissue disorders claim 3; Page 75-77; 120pp; English.

This sequence represents the murine derived protein, osteogenic protein, mOP-2. The mature OP-2 protein was used as at least one subunit in the dimeric protein of the invention. This absociated to give a structure with morphogenic activity. Each subunit comprises more than 100 amino acids having a pattern of
                                                                                                                                                                                                                                                    Maintaining integrity of gastrointestinal lining using a morphogen (stimulant) - for treating or preventing ulceration, also to inhibit endothelial cell proliferation and reduce side
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subunit; dimer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 118; DB 10; Length 399
Pred. No. 4.60e+00;
12; Mismatches 22; Indels
                                                                                                                                    Oppermann H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
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                                                                                                                                Kuberasampath T, C
leger DC, Smart JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oppermann H,
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04.MAR-1993; US-029335.
31.MAR-1993; US-040510.
(CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                  Rueger DC,
15-SEP-1992; US-945286.
04-MAR-1993; US-029335.
31-MAR-1993; US-040510.
(CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R47253 standard; Protein; 399 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.4%;
Best Local Similarity 38.7%;
Matches 24; Conservative
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                                                                                                                                    Cohen CM,
                                                                                                                             Charette MF, Cohen CM, Ozkaynak E, Pang RHL, WPI; 94-118121/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cysteine residues characteristic of the morphogen family. Each subunit comprises a mature form of a subunit of a member of the morphogen family, non-covalently complexed with a peptide comprising a pro-region of a morphogenic family member, to form a complex more soluble in aqueous solvents than the uncomplexed subunits. The dimeric protein is useful in a therapeutic composition, pref. also containing a symptom-alleviating co-factor. The protein and corresponding antibody may be used in diagnostic assays, eg. to quantitate the amount of mature and soluble forms of morphogenic
                                                                                                                                                                                                                                                                                12 glalcalggghgprpp-htc-pgrrlg-arerrdmgreilavlglpgr-prpragpaaar 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of morphogen(s), e.g. osteogenic proteins, on dentinal surfaces - for inducing dentine morphogenesis, desensitising teeth or sealing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glalcalggghgprpp-htc-pqrrlg-arerrdmqrellavlglpgr-prpragpaaar 67
                                                                                                                                                                                                                                                 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse embryo full-length osteogenic protein Op-2 (W00239)
Mouse embryo full-length osteogenic protein Op-2 (W00239)
Includes a pro-sequence and the morphogenically active mature
Includes a pro-sequence (see also W00224) that includes a 7-cys C-terminal
domain. Op-2 can be expressed from intact or truncated cDNA
(T33444) in prokaryotic or eukaryotic host cells. Mature Op-2 and
other morphogens (see also W00221-35), partic. human Op-1 (W00221),
can be used to induce dentine morphogenesis, to seal dental
cavities and to desensitise teeth to pressure and/or temp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Morphogen; osteogenic protein; dentine; tooth decay; caries; morphogenesis; odontoblast; 0P-2.
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                                                                                                                                                                                                            Length 399;
                                                                                                                                                                                                                                               12; Mismatches 22; Indels
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288..399
/label- 7-Cys_C-terminal_domain
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Pred. No. 4.60e+00;
                                                                                                                                                                                                             Score 118; DB 9;
Pred. No. 4.60e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Sig_peptide
18..260
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01-MAR-1995; US-396930.
(CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein; 399 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Charette MF, Rutherford RB;
WPI; 96-412583/41.
                                                                                                                                                                                                             1.4%;
Local Similarity 38.7%;
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Local Similarity 38.7%;
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                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                             399 AA;
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                                                                                                                                                             proteins produced
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Treausing for compounds which modulate morphogen expression - by incubating in the presence of epithelial cells which contain a cellular gene for morphogenic protein expression

Disclosure: Columns 67-70; 49pp; Engilsh.

The present sequence represents a mouse osteogenic proteins. Morphogens of the present sequence represents a mouse osteogenic proteins. Morphogens are inactive when reduced, but are active as oxidised homodimers and when coxidised with other morphogens (e.g. Wi8683-62). Comparison of the amino coxidised with other morphogens (e.g. Wi8683-62). Comparison of the amino coxidised with other morphogens (e.g. Wi8683-62). Comparison of the amino coxidised with other morphogens (e.g. Wi8683-62). Comparison of the amino coxidised with other morphogens (e.g. Wi8683-62). Comparison of the correction only in embryogenesis, but also in tissue and correction or only in embryogenesis, but also in tissue and correction or mammals. They induce a developmental correction of a cellular gene encoding a naturally occurring morphogenic correction of a cellular gene encoding a naturally occurring morphogenic protein. The candidate compound is incubated with epithelial cells which express the cellular gene. A change in the level of the protein cells are assayed for the presence of or the amount of the protein cells are assayed for the presence of or the amount of the protein correction or identify compounds which can increase or decrease morphogen correction or levels. Such compounds can be used in the treatment of, cells and cirrhosis of the liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                 10-MAR-1998 (first entry)
Full length sequence of mouse osteogenic protein 2 (hOP-2).
Mouse osteogenic protein; OP; OP-2; morphogen; morphogenic protein; embryogenesis; organ maintenance; tissue-specific morphogenesis; arthritis; emphysema; osteoporosis; cirrhosis.
                                                                                                                                                                                                /note= "pro region which is cleaved to yield the mature morphogenically active protein"
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12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ozkaynak E;
                                                                                                                                                                                                                                                                                                 /note= "conserved 7 Cys skeleton"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oppermann H,
                                                                                                                                                                                                                               261..399
/note= "mature protein"
                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          (CREA-) CREATIVE BIOMOLECULES INC.
W36856 standard; Protein; 399 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cohen CM, Kuberasampath T, Oj
Pang WH, Rueger DC, Smart JE;
WPI; 97-384665/35.
N-PSDB; T97882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.4%;
Best Local Similarity 38.7%;
Matches 24; Conservative
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30-AUG-1991; US-752764.
30-AUG-1991; US-752861.
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20-JUL-1994; 278729.
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                      W36856;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morphogen-induced periodontal tissue regeneration - used in integrating as implanted tooth in tooth socket or to inhibit tissue loss associated with periodontal disease or injury claim 28-29; Page 100-103; 132pp; English.

Morphogens comprising an amino acid sequence sharing at least 70% homology with DoP-1, OP-2, CBMPS, Vgl(fx), Vgr(fx), DPP(fx), GDF-1(fx), 60A(fx) and at least 80% homology with BMP3(fx), BMP5(fx) and bMP6(fx) are useful for integrating an implanted vich benindontal disease or injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= b
/note= "contains conserved 7 cysteine skeleton"
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Pred. No. 4.60e+00;
12; Mismatches 22; Indels
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15-SEP-1993; U08742.

15-SEP-1993; US-945285.

04-MAR-1993; US-040510.

31-MAR-1993; US-040510.

(CREA - CREATIVE BIOMOLECULES INC.

COHEN CM, RUBETSAMPATH T, OPPERMANN H, OZKAYNAK E;

PANG RHL, RUGGET DC, SMART JE;

WPI; 94-118107/14.
                                                                                                                               OP-1; OP-2; CBMP2; Vgl(fx); Vgr(fx); DPP(fx); GDF-1(fx); GOA(fx); BMP3(fx); BMP5(fx); BMP6(fx); tooth socket; alveolus; osteogenic protein; morphogen; morphogen; protein; periodontal tissue; regeneration; tooth implant; integration; inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-1991; US-752764.
30-AUG-1991; US-752764.
30-AUG-1991; US-752059.
(CREA-) CREATIVE BIOMOLECULES INC.
Cohen CM, Kuberasampath T, Oppermann H, Ozkaynak E;
PROF RLL, Rueger DC, Smart JE;
PROF SALL, Rueger DC, Smart JE;
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/note= "mOP-2-PP"
873..1289
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R33411;
15-JUL-1993 (first entry)
Murine pro-OP-2-PP.
T 14
R57974 standard; Protein; 399 AA.
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Best Local Similarity 38.7%;
Matches 24; Conservative
                                               R57974;
11-OCT-1994 (first entry)
Murine OP-2.
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18-MAR-1993.
28-AUG-1992; U07358.
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                                                                                                                                                                                                                                                                         Mus musculus
WO9406399-A.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Mon Dec 28 07:52:22 1998; MasPar time 58.82 Seconds 742.293 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-951-733-20 (1-1154) from US08951733.pep 8624 1 HASGRCVILRTWEALAPAT.....TALEAAANPALPSDFKTILD 1154 Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

320804 seqs, 37834689 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-pending 1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84 9:U85 10:U86 11:U87 12:U88 13:U89 14:U90 15:U91 16:NEWP 17:NEWUG 18:NEWUG 19:NEWUG

Mean 40.462; Variance 196.348; scale 0.206 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SOFTWARES				
Result No.	Score	Query	Length	DB	TD 01	Description		Pred No.	
7	8624	100.0	1154	13	US-08-951-	Sequence 20, App.	Applicati	0.00e+00	
7	8607	8.66	1189	18	US-08-974-		Applicat	0.00e+00	
m	8607	99.8	1189	13	US-08-911-	34, 4	Applicati	0.00e+00	
4	8607	99.8	1189	13	US-08-912-	325,	Applicat	0.00e+00	
'n	8607	99.8	1200	18	US-08-974-	612,	Applicat	0.00e+00	
φ	8607	99.8	1200	13	US-08-912-	324,	Applicat	0.00e+00	
7	8607	99.8	1200	13	US-08-911-	33,	Applicati	0.00e+00	
80	8607	99.8	1285	18	US-08-974-	600,	Applicat	0.00e+00	
თ	8607	8.66	1285	13	US-08-911-	32, 4	Applicati	0.00e+00	
10	8607	99.8	1285	13	US-08-912-	314,	Applicat	0.00e+00	
11	8590	99.6	1407	13	US-08-911-	Sequence 55, Applicati	licati	0.00e+00	
12	8590	99.6	1407	18	US-08-974-	628,	Applicat	0.00e+00	
13	8590	99.6	1407	13	US-08-912-	334,	Applicat	0.00e+00	
14	8465	98.2	1132	18	US-08-974-	2, Ap	Applicatio	0.00e+00	
12	8465	98.2	1132	13	US-08-912-	'n	Applicatio	0.00e+00	
16	8465	98.2	1132	13	US-08-911-	Seguence 2, Appl	Applicatio	0.00e+00	
17	8465	98.2	1132	14	US-09-042-	Sequence 3, Appl	Applicatio	0.00e+00	
18	8465	98.2	1132	14	US-09-052-	Sequence 2, Appl	Applicatio	0.00e+00	
19	8465	98.2	1132	12	US-08-854-	225	Applicat	0.00e+00	
20	8465	98.5	1154	13	US-08-912-	323,	Applicat	0.00e+00	
21	8465	98.2	1154	18	US-08-974-	611,	Applicat	0.00e+00	

22 8465 98.2 1154 13 US-08-911- Sequence 45, Applicati 0.00e+00 24 8448 98.0 1132 14 US-09-0265Sequence-3,-Applicatio0.00e+00 25 1132 18 US-08-954- Sequence 14, Applicati 0.00e+00 26 5742 66.6 807 13 US-08-951- Sequence 14, Applicati 0.00e+00 27 5742 66.6 807 13 US-08-911- Sequence 19, Applicati 0.00e+00 27 5742 66.6 807 13 US-08-911- Sequence 5, Applicati 0.00e+00 28 5334 61.9 1003 12 US-08-974- Sequence 5, Applicati 0.00e+00 30 12 US-08-974- Sequence 5, Applicati 0.00e+00 30 12 US-08-974- Sequence 5, Applicati 0.00e+00 30 12 US-08-974- Sequence 217, Applicati 0.00e+00 31 US-08-974- Sequence 217, Applicati 2.37e-199 31 US-08-974- Sequence 217, Applicati 2.37e-199 32 US-08-974- Sequence 210, Applicati 2.37e-179 US-08-974- Sequence 2	RESULT 1 XX X	CORRESPEZ AMORESS: ADDRESSE: ADDRESSE: ADDRESSE: AMORING Center Drive CITY: Thousand Oaks STRET: One Amgen Center Drive CITY: Thousand Oaks STRET: O.A COUNTRY: USA ZIP: 91320-1789 COMPUTER: ELAPPY disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/O8/951,733 FILING DATE: 16-OCT-1997 FILING DATE: 11-JUN-1997 PRIOR APPLICATION NUMBER: US 08/873,039 FILING DATE: 11-JUN-1997 PRIOR APPLICATION NUMBER: US 08/751,189 FILING DATE: 11-JUN-1997 REGISTRATION NUMBER: 34,688 REGISTRATION NUMBER: A-433B TELECOMMUNICATION INFORMATION: NAME: Oleski, Nancy A, R88 REGISTRATION NUMBER: A-433B TELECOMMUNICATION INFORMATION: REPERBRECE/DOCKET NUMBER: A-433B TELECOMMUNICATION INFORMATION: TELEPHONE: (805) 447-6604 TELEFAX: (805) 447-6604
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                                                 Length 1154;
                                                            Indels
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                                                Score 8624; DB 13;
Pred. No. 0.00e+00;
                                                            0; Mismatches
                              LE TYPE: protein
1154 AA; 129326 MW; 6842246 CN;
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino acids
                  unknown
                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1154; Conservative
                        unknown
           TYPE: amino acid
STRANDEDNESS: unk
TOPOLOGY: unknown
                              MOLECULE TYPE:
                                    SEQUENCE
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KGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAA
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APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Raren B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSONA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                         1189 AA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911 217
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/974,549
FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 613, Application US/08974549
                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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CLASSIFICATION:
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ID US-08-974-549-613
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722 ODPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAF 781
  482 QVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAW 541
                                                                                                                                  637 VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYV
                                                                                                                                                          1022 NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK
                                                                        VGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA
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                                              577 LRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William
TILLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
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US-08-911-312-34
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Pred. No. 0.00e+00;
0; Mismatches 1; Indels 0;
                                                                                                    PAPELICATION NUMBER: US 08/915,503
FILING DATE: 14-MG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R INFORMATION: hTRT protein"
1189 AA; 133179 MW; 7256545 CN;
                                            US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                 FILING DATE: 14-AUG-PRIOR APPLICATION DATA:
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Best Local Similarity 99.9%;
Matches 1152; Conservative
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LOCATION: 1..1189
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid STRANDEDNESS:
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LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 1056
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                                                  517 QVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAW 576
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                                                                                                                                                                                                                                 LRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS
                                                                                                                                                                                                                                                 VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYV
                                                                                                457 HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
                                                                                                                                                                                   877 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
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Lingner, Joachim
Nakamura, Toru
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APPLICANT:
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Pred. No. 0.00e+00;
0; Mismatches 1; Indels 0;
                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,312 FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002500US
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LE TYPE: protein
1189 AA; 133179 MW; 7256545 CN;
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1189 amino acids
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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Best Local Similarity 99.9%;
Matches 1152; Conservative
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                                                                                         GARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA 336
                                                                                                                                                    EEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKE 396
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            APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin H
APPLICANT: Harley, Calvin H
APPLICANT: Andrews, William H
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1189;
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                                                                                                                                                                                                                                                                     #1.30
                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP
STREEF: Two Embarcadero Center, 8th Floor
TITY: San Francisco
STATE: California
                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 8607; DB 13;
Pred. No. 0.00e+00;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HENCE 1189 AA; 133179 MW; 7256545 CN;
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CLASTICCATION: ~___
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
FILING DATE: 01-0CT-1996
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                               United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION UNDRER: 36,429
REFERENCE/DOCKET NUMBER: 0153E
TELECOMMUNICATION INFORMATION:
TELEFRA: (415) 576-0200
INFORMATION FOR SEQ ID NO: 325:
SEQUENCE CHARACTERISTICS:
Chapman, Karen B.
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1189 amino acids
                                                                                                                                                                                                         COMPUTER READABLE FORM:
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Best Local Similarity 99.9%;
Matches 1152; Conservative
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E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor

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48 ASTQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV 107
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                                                                                                                                                                    99.8%; Score 8607; DB 18; Length 1200; 99.9%; Pred. No. 0.00e+00;
                                                                                             /note= "fusion protein composed of
and Anti-Xpress tags, enterokinase
cleavage site and full length hTRT
                                                                                                                                                                                             1; Indels
                                                                                                                                                                                             0; Mismatches
                                                                               LOCATION: 1.1200
OTHER INFORMATION: /note= "fusion proTHER INFORMATION: and Anti-Xpress to OTHER INFORMATION: cleavage site and OTHER INFORMATION: protein"
NCE 1200 AA; 134322 WW; 7387257 CN;
1200 amino acids
                                               MOLECULE TYPE: protein
                                                                                                                                                                               Best_Local Similarity 99.9%;
Matches 1152; Conservative
                                                                      NAME/KEY: Protein
            amino acid
                                     linear
                     STRANDEDNESS:
                                    TOPOLOGY:
 LENGIH:
                                                                                                                                             SEQUENCE
                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 EEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKE 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 VLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1200;
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Pred. No. 0.00e+00;
0; Mismatches 1; Indels
FILING DATE: 25-APR-1997
CLASSIFICATION 435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATE: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION 3A15
PRIOR APPLICATION 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTATION UNMERE: 36,429
REFERENCE/DOCKET WUMBER: 015389-002600US
TELEFAN (415) 576-0200
TELEFAN (415) 576-0300
INFORMATION CRASS (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                             JE TYPE: protein
1200 AA; 134322 MW; 7387257 CN;
                                                                                                                                                                                                                                                                                                                       LENGTH: 1200 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.9%;
Matches 1152; Conservative
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APPLICANT: Cech, Thomas R.
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Andrews, William H.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STARET: California
                                                                                                                                                                                                                                                                                                        1008 LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 1067
                                                                                                                                                                       1068 NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1127
                                                                                                                                                                                                                                         1128 GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1187
                                                                                     AKTFLRTLVRGVPEYGCVVVLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT 1007
                                                                                                                      961
                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Plan PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
FRIENG BATE: 06-MAY-1997
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1200 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 324, Application US/08912951 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 324, Application US/08912951
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                               KSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR
                                                                                                           AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT
                                                                                                                 QDPPPELYFVKVDVTGAYDT1PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAF
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CANTENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                       1200 AA.
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                                                                                                                                                                                                                                                                                                         Sequence 33, Application US/08911312
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                                                                                                                                                                                                                                                                        PRIOR AFFLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-NG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-NG-1997
ATTORNEY/AGENT INFORMATION:
NAME: BINDAIN, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002500US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 8607; DB 13;
Pred. No. 0.00e+00;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
FENCE 1200 AA; 134322 MW; 7387257 CN;
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
                                                                                               APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1200 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 99.8%;
Best Local Similarity 99.9%;
Matches 1152; Conservative
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/note= "fusion protein composed of
enterokinase cleavable, His tagged
thioredoxin moiety and full length
) MW; 8449280 CN;
                                                                                                                Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                      CLASSETCATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-00-01-1996
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 05-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 101-OCT-1997
APPLICATION NUMBER: PCT/US97/17618
FILING DATE: 101-OCT-1997
APPLICATION NUMBER: PCT/US97/17618
FILING DATE: TOT-1997
APPLICATION NUMBER: PCT/US97/17618
FILING DATE: TOT-1997
APPLICATION NUMBER: PCT/US97/17618
FILING DATE: TOT-1997
                                                                                                                      SOFTWARE, CONTROL DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549
FILING DATE: 19-NOV-1997
                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1285 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: en OTHER INFORMATION: en OTHER INFORMATION: th INCE 1285 AA; 143529 M
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 San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Protein LOCATION: 1..1285
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Matches 1152; Conser
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                                                                                                                   SOFTWARE:
                          COUNTRY:
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                                                                                                                               VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYV 707
                                                                                                                                                             661
                                                                                                                                                                                         VGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA 767
                                                                                                                                                                                                       IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH
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                                                                  588 LRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS
          528 QVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Human Helomerase Catalytic Subunit NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNOOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: NAKAMURA, Toru
APPLICANT: Chapman, Karen B.
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APPLICANT:
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1142 NPALPSDFKTILD 1154
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                                                                                                                                            EEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKE
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                                                                     VLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAP
                 62 QRGDPAAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAF
                                   GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF
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APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENITON: Telomerase Reverse Transcriptase NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

APPL
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REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002500US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
                                PRT;
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                                                                                                                                                                                                                         Sequence 32, Application US/08911312
                                                                                                                                                                         Sequence 32, Application US/08911312
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INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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                                STANDARD;
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ZIP: 94111-3834
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                                                                        193 QRGDPAAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAF 252
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                        Length 1285
                                    Indels
                       Score 8607; DB 13;
Pred. No. 0.00e+00;
0; Mismatches 1;
     LE TYPE: protein
1285 AA; 143529 MW; 8449280 CN;
                       Query Match

Best Local Similarity 99.9%;
Matches 1152; Conservative
TOPOLOGY: linear
      MOLECULE
           SEQUENCE
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APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Linguer, Joachim
APPLICANT: Ankamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Marin, Gregg B.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND TITLE OF INVENTION: HERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
ANDRESSER
                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: U4-Aug-1997
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PRIOR APPLICATION DATA:
APPLICATION UNDBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
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: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08912951
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 314, Application US/08912951
                                                                                                                                                                                                                                                                                                                                     STANDARD;
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MEDIUM TYPE: Floppy
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1082 GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1141
 973 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH
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CURRENT APPLICATION DATA:
PELLCATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Revinmer OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08911312
                                                                                                                                                                                                                                                                                                                                                                            Sequence 55, Application US/08911312
                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                               1273 NPALPSDFKTILD 1285
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US-08-911-312-55
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                                                                                                                                                                        Length 1285;
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                                                                                                                                                                      Score 8607; DB 13;
Pred. No. 0.00e+00;
0; Mismatches 1;
                 REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 314:
SEQUENCE CHARACTERISTICS:
                                                                                                                                     MOLECULE TYPE: protein
ENCE 1285 AA; 143529 MW; 8449280 CN;
                                                                                              LENGTH: 1285 amino acids
ATTORNEY/AGENT INFORMATION:
           Randolph
                                                                                                                                                                     Query Match 99.8%;
Best Local Similarity 99.9%;
Matches 1152; Conservative
                                                                                                         amino acid
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         NAME: Apple,
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                                         VGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gareg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERAIING SYSTAM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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US-08-974-549-628
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                                  PRICIA APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY AGENT INFORMATION:
NAME: E1hhorn, Gregory P.
REGISTATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 01389-002500US
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-020
TELEFAX: (415) 576-020
INFORMATION FOR SEC 1D NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                   Score 8590; DB 13;
Pred. No. 0.00e+00;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
FENCE 1407 AA; 157668 MW; 10134798 CN;
            APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acids
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.6%;
Best Local Similarity 99.7%;
Matches 1150; Conservative
                                                                                                                                                                                                                                                                                                     amino acid
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1095 IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 1154
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                                                                              242 GARRRGGSASRSLPLPRKRPRRGAAPEPERTPVGQCSWAHPGRTRGPSDRGFCVVSPARPA
                                                                                                                                            KSHVSTLTDLQPYMRQFVAHLQETSPLRDAVV1EQSSSLNEASSGLFDVFLRFMCHHAVR
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                                                                                                                            EEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKE
                                                                                                                                                                                          QLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
                                                                                                                                                                                                                                                      HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
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US-08-912-951-334
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Pred. No. 0.00e+00;
1; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 015389-002610US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAX-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-MG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
                                                                                                                       FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 06-MAY-1997
                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
US/08/974,549
                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 628:
SEQUENCE CHARACTERISTICS
LENGTH: 1407 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
              19-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.6%;
Best Local Similarity 99.7%;
Matches 1150; Conservative
APPLICATION NUMBER:
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OTHER INFORMATION:
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                             CLASSIFICATION:
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                                                                                               APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Callyin
APPLICANT: Harley, Callyin
APPLICANT: HILL OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
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Pred. No. 0.00e+00;
1; Mismatches 2;
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NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DCOKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
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1407 AA; 157668 MW; 10134798 CN;
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18 APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
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APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MX-1997
CLASSIFCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
                                                                        Sequence 334, Application US/08912951
GENERAL INFORMATION:
                                            Sequence 334, Application US/08912951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 334.
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.6%;
Best Local Similarity 99.7%;
Matches 1150; Conservative
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Length 1132;

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83 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTISVR 142
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                          NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
                                                                                                                                                                                                                  Query Match 98.2%; Score 8465; DB 18;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 1132; Conservative 0; Mismatches 0;
                                                                                                                                                                           MOLECULE TYPE: protein
JENCE 1132 AA; 126995 MW; 6588209 CN;
               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
  FILING DATE:
                                                                                                                                                                                         SEQUENCE
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1082 GAAGPLPSEAVQWICHQAFLLKITRHRYTYVPLLGSLRTAQIQLSRKLPGTTLTALEAAA 1141
                                                                                                                                                                                                                        Sequence 2, Application US/08974549
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Garega B.
APPLICANT: Morin, Garega B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/974,549
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
FILING DATE: 10-08/08/14,419
FILING DATE: 10-08/08/14,419
FILING DATE: 10-08/08/14,419
                                                                                                                                                                                                                                                                                                                                                                                          E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                        1132 AA.
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FILING DATE: 01-0CT-1997
PRIOR APPLICATION DATA: APPLICATION NUMBER: WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRICATION DATA:

APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APP-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
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14-AUG-1997
                                                                                                                        PRT;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                      STANDARD;
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STATE: California
                                    USA
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US-08-974-549-2
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TOPOLOGY: 1:
MOLECULE TYPE:
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APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Harley, William H.
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOwnserd
                                                                                             1020
                                                                                                     1043 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1102
                         960
                                                                   803 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL
                                                           RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF
                                                                                             NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP
                                                                                                                               FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL
1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
                                                                                                                                                                        ZIE: 9411
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  1132 AA
                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crev
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AdG-1997
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
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FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                     Sequence 2, Application US/08912951
                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                 US-08-912-951-2
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
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Pred. No. 0.00e+00;
0; Mismatches 0;
                                                                                                                                                                                             015389-002600US
   FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATE: APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY APPLICATION: 435
ATTORNEY AFFERM
                                                                                                                                                                                                                                                                                                                                                          LE TYPE: protein
1132 AA; 126995 MW; 6588209 CN;
                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 0153E
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 98.2%;
Best Local Similarity 100.0%;
Matches 1132; Conservative
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Matches 1132; Conservative
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683 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI 742
                                                                      862
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                                                             LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL
                                                                                                RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF
                                                                                                                                   NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP
                                                                                                                                                                     PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL
                                                                                                                                                                                                                                1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
                                                                                                                                                                                                                                          1103 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAANPALPSDFKTILD 1154
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase
CORRESPONDENCE: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/911,312
FILING DATE: 14 AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                      1132 AA
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08911312 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08911312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RY: USA
94111-3834
                                                                                                                                                                                                                                                                                     US-08-911-312-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 MPRAPRCRAVRSLLRSHYREVIPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 82
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                                                                                                                                                                                                                                                                                                                     NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFENCE/DOCKET NUMBER: 015389-002500US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 8465; DB 13;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 1132 AA; 126995 MW; 6588209 CN;
                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                          FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                           US 08/912,951
                                                                                                                                              FILING DATE: 09-MAY-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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Local Similarity 100.0%;
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61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 SYLPNTVTDALKGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..1132 /note= "human telomerase reverse OTHER INFORMATION: transcriptase (hrRT)" (CTER 1132 AA; 126995 MW; 6588209 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 8465; DB 14;
Pred. No. 0.00e+00;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Einhorn, Gregory P.
REGISTRARION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-003110US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                     PELLING DATE: 14-NOG-159/
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-NOG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 10-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION NUMBER: US 08/979,742
FILING DATE: 10-NOV-1997
APPLICATION NUMBER: US 08/979,742
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 08/979,742
ATPLICATION NUMBER: US 08/979,742
ATPLICATION NUMBER: US 08/979,742
ATPLICATION NUMBER: US 08/979,742
ATPLICATION NUMBER: US 08/979,742
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAX-1997
FILING DATE: 06-MAX-1997
FILING DATE: 06-MAX-1997
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1132 amino acids
                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.2%;
Best Local Similarity 100.0%;
Matches 1132; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                              NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP 1020
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                                                                                                                                                                                                                                                                                       LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI
                                                                                                                                                    PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL
                   601 LSEAEVROHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA
                                                                                                      Sequence 3, Application US/09042460
GENERAL INFORMATION:
APPLICANT: Morin, Gregg B.
APPLICANT: Alisopp, Richard
APPLICANT: Depinho, Ronald
APPLICANT: Grenberg, Roger
TILLE OF INVENTION: Mouse Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1081 KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/042,460 FILING DATE: 16-MAR-1998 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor STATE: San Francisco STATE: California
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APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09042460
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ZIP: 94111-3834
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ID US-09-042-460-3
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APPLICANT: Cach, Thomas R.
APPLICANT: Cach, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and
TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                              Townsend and Crew LLP Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: WO PCT //ICCT
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,919
FILING DATE: 31-MAR-1998
CLASSIFETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: US 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us 08/911,312
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APPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                      Sequence 2, Application US/09052919
GENERAL INFORMATION:
Sequence 2, Application US/09052919
                                                                                                                                                                                                            ADDRESSEE: Townsend and
STREET: Two Embarcadero
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 14-AUG-1997
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APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
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                         GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG
                                                                                                                                                                                                RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF
           ATQARPPPHASGPRRIGCERAWNHSVREAGVPLGLPAPGARRGGSASRSLPLPKRPRR
                                                                  GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG
                                                                                                                        RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL
                                                                                                                                                                                VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT
                                                                                                                                                                                                                                       PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI
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ID US-09-052-919-2
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NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DGORET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                          Sequence 225, Application US/08854050 GENERAL INFORMATION:
                                                                                                                                                                                                          Sequence 225, Application US/08854050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08 FILING DATE: 01-0CT-1996 CLASSIFICATION: 536
                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-1997
N: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 25-APR-CLASSIFICATION: 536
PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 06 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                    US-08-854-050-225
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                                                                                                                                           61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120
                                                                                                                 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                      ATQARPPHASGPRRIGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS
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                                                                    Length 1132;
                                                                                        Indels
                                                                     Score 8465; DB 14;
Pred. No. 0.00e+00;
                                                                                      0; Mismatches
                                            LE TYPE: protein
1132 AA; 126995 MW; 6588209 CN;
       SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
INFORMATION FOR SEQ ID NO:
                                                                    Query Match 98.2%;
Best Local Similarity 100.0%;
Matches 1132; Conservative
                                   linear
                                         MOLECULE TYPE:
                                  TOPOLOGY:
                                                    SEQUENCE
                                                                                                                                                                                                                                 203
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NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLLQAYRFHACVLQLP
                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050 FILING DATE: 09-MAY-1997 CLASSIFICATION: 536
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 536
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATE: US 08/724,643
                                                                                                                                          STANDARD:
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FILING DATE: 25-APR-1997
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PRIOR APPLICATION DATA:
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                                                                         Length 1132;
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                                                                       Score 8465; DB 12;
Pred. No. 0.00e+00;
0; Mismatches 0;
                                        TOPOLOGY: linear
MOLECULE TYPE: protein
HENCE 1132 AA; 126995 MW; 6588209 CN;
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225
SEQUENCE CHARACTERISTICS:
                             LENGTH: 1132 amino acids
                                                                       Query Match 98.2%;
Best Local Similarity 100.0%;
Matches 1132; Conservative
                                    TYPE: amino acid
                                                         SEQUENCE
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DIAGNOSTIC AND
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APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Morin, Greeg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIA
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                         RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF
                                                                                             NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
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CITY: San Francisco
STATE: California
COUNTRY: United States of Americ
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US-08-974-549-611
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                                                                                                                                         Length 1154;
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             ATTORNEY AGENT INFO TO THE TO THE TOTAL TO THE TELETRATION INFORMATION:

TELETRENCE/COCKET NUMBER: 015389-002600US

TELETRENCE/COCKET NUMBER: 015389-002600US

TELETRENCE/COCKET NUMBER: 015389-002600US

TELETRENCE/COCKET NUMBER: 015389-002600US

TELETRENCE (415) 576-0300

INFORMATION FOR SEQ ID NO: 323:
SEQUENCE CHARACIERISTICS:
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                                                                                                                                         Score 8465; DB 13;
Pred. No. 0.00e+00;
                                                                                                                                                         0; Mismatches
                                                                                                                  MOLECULE TYPE: protein
FENCE 1154 AA; 129603 MW; 6816882 CN;
                                                                                   LENGTH: 1154 amino acids
01-OCT-1996
                                                                                                                                         Query Match 98.2%;
Best Local Similarity 100.0%;
Matches 1132; Conservative
                                                                                            amino acid
                                                                                                            linear
FILING DATE: 01 CLASSIFICATION:
                                                                                                   STRANDEDNESS:
                                                                                                            TOPOLOGY:
                                                                                                                           SEQUENCE
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                   LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL
                                                                                                 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF
                                                                                                                                                                                                                                             NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLLQAYRFHACVLQLP
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QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Grogg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/R51 P42
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
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APPLICATION NUMBER: US 08/1
FILING DATE: 13-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
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STREET: Two Embarcadero
CITY: San Francisco
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PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "fusion protein composed of hTRT protein sequence, vector sequences, the Myc epitope and His6 tag" MW; 6816882 CN;
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Pred. No. 0.00e+00;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                      NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                                                                         APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILLING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                               APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/912,951
                                                                                      FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
PRIOR APPLICATION NUMBER: US 08/915,503
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 611:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       1154 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                      vuery match
Best Local Similarity 100.0%;
Matches 1132; Conservative
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MOLECULE TYPE: protein
                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1.1154
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Protein
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                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE
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                                                         RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI
                                                                                                                                                                                                                                                                                                           LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI
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APPLICANT: Cech, Thomas R.
APPLICANT: Chapman, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morih, Gregg B.
APPLICANT: Morih, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Fandrews, William
IITLE OF INVENTION: Telomerase Reverse Transcriptase
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLP
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RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL
             PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS
                                                                                                                                                                    RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI
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GENERAL INFORMATION:
APPLICANT: Counter, Christopher M.
APPLICANT: Meyerson, Matthew
APPLICANT: Weinberg, Robert A.
TITLE OF INVENTION: Telomerase Catalytic Subunit Gene and
NUMBER OF SEQUENCES: 52
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                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 8465; DB 13;
Pred. No. 0.00e+00;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              015389-002500US
                                                                                                                                                                                                                                   FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
SEQUENCE 1154 AA; 129603 MW; 6816882 CN;
                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
                                                                                                  SUTREMENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Einhorn, Gregory P.
REGISTATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 01536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1154 amino acids
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Best Local Similarity 100.0%;
Matches 1132; Conservative
California
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                          94111-3834
                                                                                                                                                     CLASSIFICATION:
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                           361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT
                                                                                     PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS
                                                                                                                                          RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRGCAWLRRSPGVGCVPAAEHRLREEI
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Greeg B.
Harley, Calvin B.
Andrews, William H
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Pred. No. 0.00e+00;
0; Mismatches 1; Indels 0;
                                                      COUNTRY: USA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPA:

OPERATING SYSTEM: PC-DOS/MS-DOS

OFFWARE: Patentin Release #1.0, Version #1.30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: WH197-11p4AM TELECOMMUNICATION INFORMATION: TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
ENCE 1132 AA; 126937 MW; 6590273 CN;
                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,762
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/054,549
FILING DATE: 01-AUG-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/064,322
FILING DATE: 30-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/047,151
FILING DATE: 20-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/038,750
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32,227
                           STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1132 amino acids
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Best Local Similarity 99.9%;
Matches 1131; Conservative
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                                         CITY: Lexi
STATE: MA
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Pred. No. 0.00e+00;
1; Mismatches 1; Indels 0;
IIILE OF INVENTION: Human Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 726
                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAX-1997
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAX-1997
PRIOR APPLICATION NUMBER: US 08/854,050
PRIOR APPLICATION NUMBER: US 08/911,312
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AGG-1997
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ENCE 1132 AA; 126950 MW; 6598565 CN;
                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
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FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/974,549
FILING DATE: 19-NOV-1997
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 344:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
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larity 99.8%;
Conservative
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                                                                         San Francisco
                                                                                        California
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                                                                                                                  ZIP: 94111-3834
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CLASSIFICATION:
                                                                                                   USA
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hes 1130; Conser
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                                                                         CITY: Sar
STATE: Ca
COUNTRY:
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                                                                                                              APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: NOVEL GENES ENCODING TELOMERASE PROTEINS
UNMER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 949;
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                                                                                                                                                                                                                                                                                                     SCHWARE: Patentin Release #1.0, Version #1.30 SCHWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,733 FILING DATE: IC-OCT-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7113; DB 13;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/873,039
FILING DATE: 11-00V-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,189
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
MOLECULE TYPE: protein
ENCE 949 AA; 106370 MW; 4628597 CN;
                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/M-DOS
SOFTWARE: PAtentIn Release #1.0, N
                                                                                                                                                                       ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
                                                                                      Sequence 14, Application US/08951733 GENERAL INFORMATION:
                                                            Sequence 14, Application US/08951733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (805) 499-8011
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (805) 447-6504
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Best Local Similarity 100.0%;
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241 PGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARP 300
                                                                                                                                                                                          EQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLG
                                                                                    NHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSP
                                                                                             WLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRK
                                                                                                                                                                  661 VVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVR
                                                                                                                                                                                                                                                                                                                                     RIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLT
                301 AEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDK
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Search completed: Mon Dec 28 07:53:25 1998 Job time : 63 secs.

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Sequence 21, Applicati
Sequence 22, Applicati
Sequence 21, Applicati

US-08-951-733-20.rai

24 125 1.4 402 1 US-08-643- Sequence 21, Appli 25 125 1.4 402 1 US-08-452- Sequence 21, Appli 26 125 1.4 402 1 US-08-452- Sequence 21, Appli 28 1.4 402 1 US-08-155- Sequence 21, Appli 29 125 1.4 402 1 US-08-155- Sequence 21, Appli 31 125 1.4 402 1 US-08-155- Sequence 21, Appli 32 125 1.4 402 1 US-08-155- Sequence 21, Appli 31 125 1.4 402 1 US-08-169- Sequence 21, Appli 31 125 1.4 402 1 US-08-169- Sequence 21, Appli 31 125 1.4 402 1 US-08-169- Sequence 21, Appli 31 125 1.4 402 1 US-08-406- Sequence 21, Appli 32 125 1.4 402 1 US-08-406- Sequence 21, Appli 31 125 1.4 402 1 US-08-406- Sequence 21, Appli 40 125 1.4 402 1 US-08-479- Sequence 21, Appli 40 125 1.4 402 2 PCT-0S93-0 Sequence 21, Appli 41 125 1.4 402 2 PCT-0S93-0 Sequence 21, Appli 41 125 1.4 402 2 PCT-0S93-0 Sequence 21, Appli 41 125 1.4 402 2 PCT-US93-0 Sequence 21, Appli 41 125 1.4 402 2 PCT-US93-0 Sequence 21, Appli 41 125 1.4 402 2 PCT-US93-0 Sequence 21, Appli 41 125 1.4 402 2 PCT-US93-0 Sequence 21, Appli 41 125 1.4 402 2 PCT-US93-0 Sequence 21, Appli 41 125 1.4 402 2 PCT-US93-0 Sequence 21, Appli 41 125 1.4 402 2 PCT-US93-0 Sequence 21, Appli 41 125 1.4 402 2 PCT-US93-0 Sequence 21, Appli 41 125 1.4 402 2 PCT-US93-0 Sequence 21, Appli 41 125 1.4 402 2 PCT-US93-0 Sequence 6, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 6, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 6, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 6, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 6, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 6, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 6, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 6, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 6, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 6, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 6, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 6, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 6, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 61, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 61, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 61, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 61, Appli 61 125 1.4 402 2 PCT-US93-0 Sequence 61, A	SULT 1 US-08-147-023 XXXXXX	Sequence Seq	CC COMPUTER READABLE FORM: CC MEDIUM TYPE: Floppy disk CC COMPUTER: IBM PC compatible CC COMPUTER: IBM PC compatible CC COMPUTER: IBM PC compatible CC CURRENT APPLICATION DATA: CC CURRENT APPLICATION DATA: CC FILING DATE: 21-FEB-1992 CC APPLICATION NUMBER: US/08/147,023 CC APPLICATION NUMBER: US/08/147,023 CC APPLICATION NUMBER: US/08/147,023 CC APPLICATION NUMBER: US/050 CC APPLICATION NUMBER: US/050 CC APPLICATION NUMBER: US/052 CC APPLICATION NUMBER: US/052 CC APPLICATION NUMBER: US/052 CC APPLICATION NUMBER: US/050 CC APPLICATION UMBER: US/0
######################################	>US-08-951-733 n: (1-1154) from ore: 8624 1 HASGORCVLLRT ble: PAM 150 Gap 11 77309 seqs, 70	rocessing: Minimum Match 0% Listing first 45 summaries a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1 Lics: Mean 37.265; Variance 182.038; scale 0.205 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being pri and is derived by analysis of the total score distribution. SUMMARIES Query Score Match Length DB ID Description 118 114 399 1 US-08-147- Sequence 27, Applicati 2. 118 114 119 114 119 114 119	118 1.4 399 1 US-0822-0 Sequence 23, Applicati 2.06e+00 5 118 1.4 399 1 US-08-278 Sequence 23, Applicati 2.06e+00 6 118 1.4 399 1 US-08-643 Sequence 23, Applicati 2.06e+00 7 118 1.4 399 1 US-08-643 Sequence 23, Applicati 2.06e+00 8 118 1.4 399 1 US-08-479 Sequence 23 Applicati 2.06e+00 118 1.4 399 1 US-08-479 Sequence 23, Applicati 2.06e+00 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 12 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 13 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 14 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 14 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 15 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 16 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 17 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 1 US-08-480 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 399 2 PCT-US93-0 Sequence 23, Applicati 2.06e+00 18 118 1.4 402 1 US-08-404 18 290 1 US-08-404 18 20 1 US-08-404 18 20 1 US-08-404 18 20 1 US-08-404 18 20 1 US-0

US-08-951-733-20.rai

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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   NOTRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
WEDIUM TYPE: IDPPPY disk
COMPUTER: IBM PC COMPATIBLE
CO
   APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/447,570
FILING DATE: 21-FEB-1992
CLASSIFICATION SATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
FILING DATE: 20-DEC-1991
FILING APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60,162
FILING DATE: 22-FEB-1991
FILING DATE: 22-FEB-1991
FILING DATE: 04-DEC-1990
FILING DATE: 04-DEC-1990
FILING DATE: 04-DEC-1990
FILING DATE: 104-DEC-1990
FILING DATE: 104-DEC-1990
FILING DATE: 104-DEC-1990
FILING DATE: 18-OCT-1990
FILING DATE: 19-OCT-1990
FILING DATE: 19-OCT-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27,829
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            12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 1.4%; Score 118; DB 1; Length 399; Local Similarity 38.7%; Pred. No. 2.06e+00; nes 24; Conservative 12; Mismatches 22; Indels
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION NUMBER: US 616,374
FILING DATE: 12-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-CCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-CCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 59,920
FILING APPLICATION DATA:
APPLICATION NUMBER: US 59,920
FILING APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 20-AUG-1990
PRIOR APPLICATION NUMBER: US 483,913
FILING DATE: 17-CCT-1989
PRIOR APPLICATION NUMBER: US 422,613
FILING DATE: 17-CCT-1989
PRIOR APPLICATION NUMBER: US 315,342
FILING DATE: 17-CCT-1989
PRIOR APPLICATION NUMBER: US 315,342
FILING DATE: 17-CCT-1989
PRIOR APPLICATION NUMBER: US 322,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION NUMBER: US 232,630
FILING DATE: US APPLICATION DATA:
APPLICATION NUMBER: US 212,630
FILING DATE: US APPLICATION DATA:
APPLICATION NUMBER: US 212,630
FILING DATE: US APPLICATION DATA:
APPLICATION NUMBER: US 212,630
FILING DATE: US APPLICATION DATA:
APPLICATION NUMBER: US 212,630
FILING DATE: US APPLICATION NUMBER: US 212,630
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MOLECULE TYPE: protein
JENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/08447570 Patent No. 5714589 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/248-7000
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 annino acids
TYPE: amino acid
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US-08-447-570-27
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Pred. No. 2.06e+00;
12; Mismatches 22; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application PC/TUS9201968
GENERAL INFORMATION:
APPLICANT: COHEN, CHARLES M
APPLICANT: FUBERASAMPATH, THANGAVEL
APPLICANT: PANG, ROY HL
APPLICANT: OPPERMANN, HERMANN
APPLICANT: RUGGER, DAVID C
TITLE OF INVENTION: PROTEIN-INDUCED MORPHOGENESIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSED: TESTA HURWITZ & THIBEAULT
STREET: EXCHANGE PLACE 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/01968
FILING DATE: 19920311
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 667,274
FILING DATE: 11-MAR-1991
PRIOR APPLICATION NUMBER: US 667,274
FILING DATE: 11-MAR-1991
PRIOR APPLICATION NUMBER: US 67,274
FILING DATE: 30-AUG-1991
ATPONENT/AGENTI INFORMATION:
AMPLICATION NUMBER: 30-AUG-1991
ATPONENT/AGENTI INFORMATION:
                                                                                                                                                                                                                                                                                                            399 AA.
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REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-052PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
TYPE: AMINO ACID
          TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                                                                                                            PRT;
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617/248-7000
                                                                                                                           Query Match
1.4%;
Best Local Similarity 38.7%;
Matches 24; Conservative
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COUNTRY: USI
ZIP: 02109
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PCT-US92-01968-23
  TELEPHONE:
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                                                                                                     SEQUENCE
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Pred. No. 2.06e+00;
12; Mismatches 22; Indels 4; Gaps
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Patent Vo. 5650276
GREEAL INFORMATION:
APPLICANT: SMART, JOHN
APPLICANT: OPPERMANN, HERMAN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: RUBEBRASMPATH, THANGAVEL
APPLICANT: COHEN, ROY CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITT: HOPKINTON
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Pred. No. 2.06e+00;
12; Mismatches 22; Indels
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COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,729A
FILING DATE: 20-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHERE BSq. EDMUND R.
REGISTRENCE/DOCKET NUMBER: 27,839
REFERENCE/DOCKET NUMBER: CRP-058CPFW
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: protein
JENCE 399 AA; 44764 MW; 790568 CN;
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/08278729A
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TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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                                                                                                                            Query Match
Best Local Similarity 38.7%;
Matches 24; Conservative
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MEDIUM TYPE: Floppy
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Best Local Similarity 38.7%;
Matches 24; Conservative
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AC XXXXX

AC XXXXX

DE Sequence 23, Applica

XX Sequence 23, Applica

CC Patent No. 5650276

CC GENERAL INFORMATION

CC APPLICANT: SPAN

CC APPLICANT: SPAN

CC APPLICANT: COHN

CC CONDUTER: DA

CC CONDUTER: DA

CC COMPUTER: TEB

CC COMPUTER: TEB

CC COMPUTER: COMPUTE
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US-07-901-703-13
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APPLICANT: KUBERAAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMANN, HERMAN
APPLICANT: OPPERMANN, HERMAN
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: MORHOGENIC-INDUCED PERIODONTAL TISSUE
TITLE OF INVENTION: RECENERATION.
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSE:
ADDRESSEE: PATERY ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 118; DB 1; Length 399;
Pred. No. 2.06e+00;
12; Mismatches 22; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,763A
FILING DATE: 06-MAY-1996
CLASSIFICATION: 514
ATYORNEY/AGENT INFORMATION:
NAME: FENTON ESq., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: 36,508
TELEPHONICATION INFORMATION:
TELEPHONICATION INFORMATION:
TELEPHONICATION 11PORMATION:
TELEPHONICATION 1248-7560
INFORMATION FOR SEQ ID NO: 23:
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MOLECULE TYPE: protein
HENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/08643763A Patent No. 5733878 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 Sequence 23, Application US/08643763A
                                                                                                                                                                                                          STANDARD;
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amino acid
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ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acid
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1.4%;
Best Local Similarity 38.7%;
Matches 24; Conservative
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                                                                                                                                                                                                        US-08-643-763A-23
                                                                                                                        254 LP 255
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12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: RUBERSAMPATH, THANGAVEL
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: COPERMANN, HERMANN
APPLICANT: OZAKAYNAK, ENGIN
TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED
TITLE OF INVENTION: OSTEOGENIC PROPERTIES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,703
FILING DATE: 19920616
CURSIFICATION: 4355
CURSIFICATION: 4355
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399 AA
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                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET EXCHANGE PLACE, 53 STATE STREET CITY: BOSTON STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
PRT;
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JENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STK-057
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                                                                                                                                             Sequence 13, Application US/07901703 Patent No. 5344654
                                                                                                           Sequence 13, Application US/07901703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 399 amino acids TYPE: AMINO ACID
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
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APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: RUBERANN, HERMAN
APPLICANT: COPERANN, HERMAN
APPLICANT: COHEN, CHARLES M.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE
TITLE OF INVENTION: REGENERATION.
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: HOPKINTON
                                                   ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 118; DB 1; Length 399;
Pred. No. 2.06e+00;
12; Mismatches 22; Indels
                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM:
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,666
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: FENTON ESG., GILLIAN M.
REGISTRATION NUMBER: 36,508
REBERBNCE/POCKET NUMBER: 36,508
REBERBNCE/POCKET NUMBER: 36,508
REBERBNCE/POCKET NUMBER: 36,508
TELEPHONE: (508) 435-9001
TELEFAS: (508) 435-901
TELEFAS: (508) 435-6951
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
TENGTH: 399 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 AA.
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MOLECULE TYPE: protein
SEQUENCE 399 AA, 44764 MW; 790568 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 38.7%;
Matches 24; Conservative
     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
                                                                                                                                                                  USA
                                                                                                                                                          COUNTRY: US
ZIP: 01748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-155-343A-23
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                                        APPLICANT: OPPERAMAN, HERMAN
APPLICANT: OPPERAMANN, ENGIN
APPLICANT: CZKAYNAK, ENGIN
APPLICANT: KUBERASAMARHY, THANGAVEL
APPLICANT: RUGER, DAVID C.
APPLICANT: PANG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
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Pred. No. 2.06e+00;
12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                        STATE: MA
CONTRY: USA
ZIP: 01748
COMPUTEN: USA
COMPUTEN: ISPE: Floppy disk
COMPUTEN: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,563A
FILING DATE: 05-MAY-1996
CLASSIFICATION: 435
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Patent No. 5652337
GENERAL INPORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZEANNAK, ENGIN
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: RUBERASAMPATH, THANGAVEL
APPLICANT: RUBERR, DAVID C.
APPLICANT: ROBGER, DAVID C.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS
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NAME: TWOMEY ESQ., MICHAEL J.
REGISTRATION UNMBER: 38,349
REFERENCE/DOCKET NUMBER: CRP-058
TELECOMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
TELEPHONE: (508) 435-901
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENTH: 399 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
ENCE 399 AA; 44764 MW; 790568 CN;
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                             SMART, JOHN
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Local Similarity 38.7%;
hes 24; Conservative
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TOPOLOGY: linear
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-479-666-10
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TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PCT-US93-05446-13
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ZIP: 01748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.4%; Score 118; DB 1; Length 399; Best Local Similarity 38.7%; Pred. No. 2.06e+00; Matches 24; Conservative 12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07231
FILING DATE: 19930729
                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: CREATIVE BIOMOLECULES, INC.
STREET: 35 SOUTH STREET
CITY: HOPKINTON
STATE: MASSACHUSETTS
                                                                                              APPLICATION NUMBER: US/08/155,343A
FILING DATE: 15-NOV-1993
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET 36,508
REFERENCE/DOCKET 136,508
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX: (617) 248-7560
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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IENCE 399 AA; 44764 MW; 790568 CN;
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GENERAL INFORMATION:
APPLICANT:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23, Application PC/TUS9307231
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ATTORNEY/AGENY INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
REPERCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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РСТ-US93-07231-23
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12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
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                                                                                                                                                                                              4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 399;
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1.4%; Score 118; DB 2; Length 399;
Best Local Similarity 38.7%; Pred. No. 2.06e+00;
Matches 24; Conservative 12; Mismatches 22; Indels
                                                                                                                                                                                           12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05446
FILING DATE: 19930608
CLASSITCATION:
ATTORNEY APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 AA
                                                                                                                                       Query Match 1.4%; Score 118; DB 2; I Best Local Similarity 38.7%; Pred. No. 2.06e+00; Matches 24; Conservative 12; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Creative BioMolecules, Inc.
STREET: 35 South Street
CITY: Hopkinton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: FITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: 8TK-057
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application PC/TUS9305446 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
JENCE 399 AA; 44764 MW; 790568 CN;
                                        TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application PC/TUS9305446
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AMINO ACID
: 399 amino acids
amino acid
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12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
                                                                                                                                                                                                                                                                                                                                MORPHOGEN-ENRICHED DIETARY COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 118; DB 2; Length 399;
Pred. No. 2.06e+00;
12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07190
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                           399 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          399 AA.
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: CREATIVE BIOMOLECULES, INC. STREET: 35 SOUTH STREET
CITY: HOPKINTON
STATE: MA
                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7100
                                                                                                                                                                                                                                                                               Sequence 23, Application PC/TUS9307190
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MORPHOGEN-ENRIVINGER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
JENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                                                    Sequence 23, Application PC/TUS9307190
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399 amino acids
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Best Local Similarity 38.7%;
Matches 24; Conservative
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                                                                                                                                         LT 13
PCT-US93-07190-23
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ZIP: 01748
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194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
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Pred. No. 2.06e+00;
12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 01748

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10520
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: OP3-INDUCED MORPHOGENESIS NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CREATIVE BIOMOLECULES, INC.
STREET: 45 SOUTH STREET
CITY: HOPKINTON
                                                                                                                         399 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,274
FILING DATE: 11-MAR-1991
PRIOR APPLICATION NUMBER: US 07/752,764
FILING DATE: 30-AUG-1991
PRIOR APPLICATION NUMBER: US 07/753,059
FILING DATE: 30-AUG-1991
PRIOR APPLICATION NUMBER: US 07/753,857
FILING DATE: 30-AUG-1991
PRIOR APPLICATION NUMBER: US 07/923,780
FILING DATE: 31-UL-1992
ATTORNEY/AGBNT INFORMATION:
NAME: PITCHER ESQ, EDMUND R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-076PC
TELECOMMUNICATION INFORMATION:
                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                                               Sequence 10, Application PC/TUS9310520 GENERAL INFORMATION:
                                                                                                                                                                                                                  Sequence 10, Application PC/TUS9310520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (508)435-9001 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 399 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.4%;
Best Local Similarity 38.7%;
Matches 24; Conservative
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STATE: MA
COUNTRY: USA
01748
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PCT-US93-10520-10
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                                                          254 LP 255
                             68 QP 69
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4; Gaps

US-08-951-733-20.rai

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12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
              TITLE OF INVENTION: NOVEL MORPHOGENIC PROTEIN COMPOSITIONS TITLE OF INVENTION: OF MATTER NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS: ADDRESSE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES, ADDRESSE: INC. STREET: 35 SOUTH STREET CITY: HOPKINTON STREET STREET: MATTER ADDRESSES ADDRESSES INC. STREET: MATTER HOPKINTON STREET STREET: MATTER ADDRESSES ADDRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 01748
COUNTRY: USA
ZIP: 01748
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07189
FILING DATE: 19930729
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 118; DB 2; 1
Pred. No. 2.06e+00;
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JENCE 399 AA; 44764 MW; 790568 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: RELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-(
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 38.7%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Job time : 62 secs.
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                                                                    PAPLICANT: COHEN, CHARLES M.
APPLICANT: COHEN, CHARLES M.
APPLICANT: CHARRETTE, MARC F.
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERANN, HERMANN
APPLICANT: OPPERANN, HERMANN
APPLICANT: SWART, JOHN E.
TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
TITLE OF INVENTION: ULCERS.
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DASTANT: POLOS/MS. DOS
COFFWANDER: DAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
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Local Similarity 38.7%; Pred. No. 2.06e+00;
nes 24; Conservative 12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/462,623

FILING DATE:
CLASSIFCATION NUMBER: U$/08/45,882

FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: 08/445,882

ATORNEY/AGENT INFORMATION:
NAME: FENTON ESq., GILLIAM M.
REGISTRATION NUMBER: 36,508

RESISTRATION NUMBER: 36,508

REFERENCE/DOCKET NUMBER: CRP-074CN

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
TENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application PC/TUS9307189 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application PC/TUS9307189
                          Sequence 23, Application US/08462623 Patent No. 5739107
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PCT-US93-07189-8
                                                        Patent No.
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ID PC
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4; Gaps

Length 399;

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(ME)
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nna n.a. • n.a. database search, using Smith-Waterman algorithm with gap extension penalties as well as gap opening penalties

Fri Dec 25 08:54:27 1998; MasPar time 9229.89 Seconds 680.010 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-951-733-13 (1-2848) from USO8951733.seq (1 of 3) 2848 Title: Description: Perfect Score: N.A. Sequence: Comp:

1 CACGCGTCCGGGCACGCTG.......GATGCCGGCCCACGGCCTAT 2848 GTGCGCAGGCCCGTCGCGAC......CTACGGCCGGGTGCCGGATA

TABLE default Gap open 30; Gap extend 1 Scoring table:

567134 seqs, 1101898692 bases x 2 Searched:

Dbase 0; Query 0

Nmatch STD:

Post-processing: Minimum Match 0% Listing first 45 summaries

emb155 Database:

1:em_ba_2:em_tun_3:em_htg_4:em_huml_5:em_hum2_6:em_in_7:em_om_8:em_or_9:em_ov_10:em_pat_11:em_ph_12:em_pl_13:em_ro_14:em_v1
13:em_ro_14:em_v1
15:gb_bal_16:gb_ba2_17:gb_htg_18:gb_in_19:gb_om_20:gb_ov_21:gb_pat_22:gb_ph_23:gb_n1_24:gb_pl_23:gb_pr_27:gb_pat_22:gb_ph_23:gb_pr_27:gb_pat_23:gb_v1_23:gb_v1_23:gb_v1_33:gb_v1_26:gb_v1_33:gb_v1_26:gb_v1_33:gb_v1_26:gb_v1_33:gb_v1_26:gb_v1

Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 11.679; Variance 6.056; scale 1.928 Statistics:

SIIMMARIES

					SUMMARIES		
		æ					
Result		Query					
NO.	Score	Match	Match Length DB	DB	ΩI	Description	Pred. No.
-	2837	9.66	4015 27	27	AF015950	Homo sapiens telomeras	0.00e+00
8	2824	99.5		31	AF043739	Synthetic construct hu	0.00e+00
e	2823	99.1		27	AF018167	Homo sapiens telomeras	0.00e+00
4	825	29.0	3426	78	AF051911	Mus musculus telomeras	_
'n	823	28.9		5 8	AF073311	Mus musculus telomeras	_
9	129	4.5	201	78	AF029235	Mus musculus telomeras	1.63e-71
7	29	2.4		21	166494	Sequence 14 from paten	
œ ن	49	1.7		21	I66494	Sequence 14 from paten	
σ	37	1.3	_	26	AC005369	Homo sapiens chromosom	
10	34	1.2		21		Sequence 5 from patent	
c 11	35	1.2	215 21	21		Sequence 5 from patent	7.37e-05
c 12	34	1.2		26		Homo sapiens chromosom	

.44e-	44e-0	.44e-0	.28e-	.95e-	je-	.50e-	že	<u>2</u> e	1.50e-01	. 59	'n	. 98e	œ	8e+		1.59e+00		4.98e+00		1.59e+00		9e+	.98e+	8e+	8e+	.98e+	4.98e+00	8e+	9e+	1.59e+00	
s gene for c DNA for		encoding enve	piens C	Mustela vison microsat	Epstein-Barr virus (wi	Methylobacterium extor	S.pombe chromosome I c		DNA sequence fr	gDNA encoding envelope	in-Barr virus		S.marcescens proBA ope		gicus s	Epstein-Barr virus (B9	S.coelicolor 6 actVA r	Azotobacter vinelandii	Pseudomonas aeruginosa	Mycobacterium tubercul	Human DNA sequence fro	Drosophila melanogaste	Homo sapiens shox gene	sedneuce	Human DNA sequence ***	*** SEQUENCING IN PROG	Homo sapiens chromosom	Human DNA sequence ***	Epstein-Barr virus (EB	Epstein-Barr virus, ar	
10.10	A10162 A10159	0407	HUAC004787	MVU92534	HS4RSIRZ2T	MEU72662	SPUNK4	SPAC2E11	HS179D3A	E04076	HS4BHLF	CHKD1LRB	SMAPROBA	SMPROBAG	AF034863	HS4U2IR2A	SCACTVA	AF027499	AF011922	ч	HSN2H6	AC004365	U82668	HS126A5	ü	\sim	3311	S	EBV	HS4B958RAJ	
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ALIGNMENTS

FO15950 4015 bp mRNA PRI 16-AUG-1997 (como sapiens telomerase reverse transcriptase (hTRT) mRNA, complete ds. PRO15950	human. human sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	nounce (bases 1 to 4015) Nakamura,T.M., Morin,G.B., Chapman,K.B., Weinrich,S.L., Andrews,W.H., Lingmar,J., Harlay,C.B. and Cech,T.R. Telomerase catalytic subunit homologs from fission yeast and human Science 277 (5328), 955-959 (1997)	9/40/0623 Vorin,G.B. Direct Submission Submitted (24JUL-1997) Geron Corporation, 230 Constitution Drive, Menlo Park, CA 94025, USA	Location/Qualifiers 1. 4015. /organism="Homo sapiens" /db_xref="taxon:9606" /tissue_type="kidney" /dev_stage="embryo" //drynoscene=="f"	/uncolored
AF015950 Homo sapiens cds. AF015950	human. Homo sapiens Eukaryotae; m Vertebrata; b	nomo. 1 (bases 1 t Nakamura, T.M. Andrews, W.H., Telomerase ca	9/400623 2 (bases 1 t Morin,G.B. Direct Submis Submitted (24 Menlo Park, C	Local 1 / Ab./ /tis/ /map/ /dev/	1 /ger 56.
RESULT 1 LOCUS 2 DEFINITION 1 ACCESSION 2	OCE CCE CGANISM		MEDLINE REFERENCE AUTHORS TITLE JOURNAL	FEATURES	gene

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AMETICCARACTEGARICACACACTAGAGGGGCCCACCACACCACCACCACCACCACGAGGCGCCGC	1812 CAMPICOLAMGATCAGGANCCACTIGANGAGGCCACCGCGGGGCCTCCT 1811 1111
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FGYLLEKCHSLELDLQWNSLQTVORIX XILLLQARREHACVLQLPHEVDQWRNDPT
LRVI SDTASLCYSILKARNAGMSYCARGANGPLPSBAVQMLCHQAFLLKLPHRVY
PLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILDYPYDVPDYAGYPYD
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b_xref="taxon:32630"
der(1. 1101,4606. 8960)
ote-"mammalian expression vector; see GenBank Accession
mber U47120"
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to 8960)
i., Meyerson,M., Eaton,E.N., Ellisen,L.W., Caddle,S.D., and Weinberg,R.A.
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2) mRNA and 3' Influenza A hemagglutinin tag, complete
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d Weinberg,R.A.
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20-JAN-1998) Whitehead Institute, 9 Cambridge Center,
MA 02142, USA
Cation/Qualifiers
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ene="hTERT/hEST2"
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anti-influenza virus hemagglutinin monoclonal antibody 12CA5; similar to part of the Influenza A hemaglutinin gene sequence in GenBank Accession Number M29257"
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/db_xref="taxon:32630"
/ 2551 c 2484 g 2038 t 1 others
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Meyerson, M., Counter, C.M., Eaton, E.N., Ellisen, L.W., Steiner, P., Caddle, S.D., Zlaugra, L., Beijersbergen, R.L., Davidoff, M.J., Liu, Q., Caddle, S.D., Zlaugra, L., Beijersbergen, R.L., Davidoff, M.J., Liu, Q., Direct Submission
Submitted (11-AUG-1997) Whitehead Institute for Biomedical Research, Massachusetts Institute of Technology, Nine Cambridge Center, Cambridge, MA 02142, USA
Location/Qualifiers
I 4027
/Organism="Homo sapiens"
/Ab_xref="taxon:9606"
Caddle, S.D., Ziaugra, L., Beijersbergen, R.L., Davidoff, M.J., Liu, O., Bacchetti, S., Haber, D.A. and Weinberg, R.A. hEST2, the putative human telomerase catalytic subunit gene, is up-requiated in tumor cells and during immortalization cell 90 (4), 785-795 (1997)
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δy	1342	TGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCC 1401
QQ	1392	GTCGCCTGGTGCTGGTCCGCCAGCACCACCCCTGGCAGGTCTACGGCTTCGT
Qy	1402	CGTCGCCTGGTGCAGCTGCTCCGCCAGCAGCAGCCCCTGGCAGGTGTACGGCTTCGTG 1461
qq	1452	GGCCTGCCTGCCGCCGGCTGGTGCCCCCCAGGCCTCCAGGCACGC 15
Qy	1462	GGGCCTGCCTGCCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACGAACG
qa	1512	CGCTICCICAGGAACACCAAGAAGTICAFCICCCIGGGGAAGCAIGCCAAGCICICGCIG 1571
Oy.	1522	GCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCT
qa	1572	CAGGACTGACGTGGAAGATGAGCGTGCGGGCTGCGCTTGGCTGCGCAGGAGCCCAGGG 1631
δλ	1582	SAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGG
q	1632	GITGGCIGTGITCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTG 1691
ΟŊ	1642	30c1G1G11CCGGCCGCAGAGCACCG1C1GCG1GAGGAGATCC1GGCCAAGT1CCT
q	1692	CACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT
Qy	1702	rgcreatgargretargregregregregretargretritititatgreacggag 17
Q	L)	ACCACGITICAAAAGAACAGGCICTITITCIACCGGAAGAGIGICIGGAGCAAGIIGCAA 1811
Qy	1762	Pacgiticaaaagaacaggcictititciaccggaagagtgtiggagcaagtig
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ογ		ITGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAG 188
qq	1872	GTCAGGCAGCATCGGGAAGCCAGGCCCGCCTGCTGACGTCCAGACTCCGCTTCATCCC 1931
Qy	1882	-AGGCAGCATCGGGAAGCCAGGCCCGCCTGCTGATCCAGACTCCGCTTCATCTCCCC 19
q	1932	AAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTC 1991
Οy	1942	CTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGGAGCCAGAACGTTC 2
đ	1992	CGAGGGTGAAGGCACTGTTCAG
Qy	2002	
đ	2052	AACTACGAGCGGCGCGCGCCCCCGGCCTCCTGGGCGCCTCTGTGCTGGGCCTGGACGAT 2111
δλ	2062	Acadecedecedecececenteresecentratere
q	2112	ATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGCGGGCCCAGGACCCGCCGCCGAG 2171
Qy	2122	ACAGGGCCTGGCGCACCTTCGTGCTGCGGGCCCCAGGACCCGCCCG
q	2172	m
Qγ	2182	INCTITGICAAGGIGGAIGIGACGGGCGCGGIACGACACCAICCCCCAGGACAGGCI
QQ	2232	ACGGAGGTCATCGCCAGCATCAACCCCAGAACACGTACTGCGTGCG
QY	2242	GGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG
q	2292	Ĕ-
QY	2302	TGGTCCAGAAGGCCGCCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCGACGTCTTA
q	2352	TTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCG 2411
Qy	2362	GACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCC
qq	41	CIGAGGAIGCCGICGICAICGAGCAGAGCICCICCGIGAAIGAGGCCAGCAGIGGCCIC 2471
δλ	2422	SAGGGATGCCGTCGTCGAGCAGAGCTCCTCCTGAATGAGGCCAGCAGTGGCCT

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al Similarity 67.1%;
1901; Conservative
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/organism="Mus musculus"
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                    TTCGACGTCTTCCTACGCTTCATGTGCCACGCCGTGCGCATCAGGGGCAAGTCCTAC
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) AAGAAGO	K K E JE J		AGCTCAG	CITGICC	GTCTAAA	AGCTGCG	TGGTGGA TCGTGGA			ATGCAGA	ACGCGCA	AACAGGT	CCCCAGC	GA.	AGGAGGA	AGGTATA	AGGTGTA	CCAGGCA	CCAGGCA	ACGGCAA	ATGCCAA				3A1CC166C2 				TCTGGAG TCTGGAG	GGGAGCTGTC 	GACTGCG 	TGGGTAC
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Martin-Rivera, L., Herrera, E., Albar, J.P. and Blasco, M.A.
Expression of mouse telomerase catalytic subunit in embryos adult tissues
Proc. Natl. Acad. Sci. U.S.A. 95 (18), 10471-10476 (1998)
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Direct Submission
Submitted (19-JUN-1998) Immunology and Oncology, Nat
Biotechnology, Cantoblanco, Madrid 28049, Spain
Location/Qualifiers
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RESULT 7 LOCUS 166494	ATGGAGAACAAGCTGTTTGCTGAGGTGCAGCGGGATGGGTTGCTTTTACGTTTTGTTGAT		7 A
QY 1924 AGACTCCGCT	4 CAGGGCATCCCCCAGGGCTCCAGCCTATCCACCTGCTGTGCAGTCTGTGTTTCGGAGAC 2523	2551	8 S
Db 181 AGACTCCGCT	1 Trectadectreaterecaceaecegreegeareagescandrectaegreerecagne 2550		οy
QY 1864 GAGCIGICGG	4 TICCTGCACTICCTGCGTCACAGTGCTGGTAAAGATTGGTGACAGGTGCTATACGCAGTGC 2463		g
Db 121 GAGCTGTCAC			ò
QY 1804 GTCTGGAGCA	4 TCCGTTGTCATCGAGCAGCATCTCTATGAATGAGCAGCAGCAGCAGCTGTTTGACTTC 2403	2344	ф
Db 61 GTGTGGAGCA		2377	οy
	4 CCATACATGGGCCAGTTCCTTAAGCATCTGCAGATTCAGATGCCAGTGCAGTGAGGAAC 2343	2284	q
Db 1 TICITITATG			ΩŽ
Best Local Similar Matches 165; Co			QQ
ORIGIN Query Match	4 ATGAICAGGCACTCGGAGAGCACGTACTGTATCCGCCAGTATGCAGTGGTCCGGAGAGAT 2223	2260	DP Qy
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HOSPITAL FEATURES Source	4 CAICCICACCITAIGGGGTCTICIGIACIGGGTAIGAAIGACAICIACAGGACCIGGCGG 2043 	1984	g &
AUTHORS Direct, R TITLE Direct, R JOURNAL SUBmittee	4 CAGCATITCACCCAGGGTCICAAGACTCTCICAGCAIGGTCAACTAIGAGGGGACAAAA 1983 	1924	ga Vy
	4 CCCATTGTGAACATGAGTTATAGCATGGGTACCAGAGCTTTGGGCAGAAGGAAG	1964	δγ
CROANISM WAS MUSCO ENWARYOUT ROGENTIA REFERENCE 1 (bases	4 ACCTGGCTAGCCATGCCCATCTGCAGACTGCGCTTCATCCCCAAGGCCCAACGGCCTGGGG 1863	1804	දු ව
	4 CACCTIGAGAGIGGGGGTACGGGAGCIGICACAAGAGGAGGICAGGCAICACCAGGC 1803 	1744	g V
	4 AGGCTCTTCTTCTACCGTAAGAGTGTGTGGAGCAAGCTGCAGAGCATTGGAGTCAGGCAA 1743 	1684	DP QY
Qy 2791 GTAGAAGACG			δλ
Db 2704 GIGGAGCCIG			3 2
DD 2644 CATGGCGTTC 	GCAGAGCACCGTCTGAGGGAGGATCCTGGCTACGTTCCTGTTCTGGCTGATGGACACA 162	1564	a B
2671	III	1600	QY OY
OY 2611 AFGGAGAACA Db 2584 GACTTTCTGT			Q
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(bases 1 to 201)
1ssi,R. and Cleveland,J.L.
rect Submission
Location/Cor-1997) Biochemistry, St jude Children's Research
spital, 332 North Lauderdale, Memphis, TN 38105, USA
Location/Qualifiers
1. 201
/organism="Mus musculus"
/db_xref="taxon:10090"
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.>201
/cell_line="32D.3"
.>201
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/codon_start=1
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/translation="FFYVTESTFOKNRIFFYRKSVWSKLQSIGVRQHLERVRLRELSQ
EEVRHHQDTWLAMPICKLRFIPK"
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ITGGTGACGCCTCACTTGGACCAAGCAAAAACCTTCCTCAGCACCCTGGTC 2643
                                                                                                               AAGTIGCAAAGCAITGGAAICAGACAGCACTIGAAGAGGGIGCAGCIGCGG 1863
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R. and Cleveland, J.L. sequence of Mus musculus telomerase catalytic subunit
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                                                                                                                                                                              Score 129; DB 28; Length 201;
Pred. No. 1.63e-71;
0; Mismatches 36; Indels (
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arity 82.1%;
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AC005369 74371 bp DNA PRI 01-AUG-1998
Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete
                                       2079 CCGCGCCCGCTGGTAGTTGAGCACGCTGAACAGTGCCTTCACCCTCGAGGTGAGACGCTC 2020
                                                                                                                                      2019 GGCCCTCTTTTCTCTGCGGAACGTTCTGGCTCCCACGACGTAGTCCATGTTCACAATCGG 1960
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                                                                                                     All Characters of the control of the
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Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Kadner,K., Miquel,T., Miller,C., Pitluck,S., Pollard,M.,
Rojeski,H., Subreamanian,S. and Martin,C.H.
Sequencing of human chromosome 5
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Large Scale Sequence Analysis and Annotation with the Sequence
Comparison Analysis (SCAN) System
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
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join(3246. .3410,3721. .3828)
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/rpt_family="Alu"
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/rpt_family-"Alu"
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'note="(GT)21"
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Pred. No. 1.13e-25;
211; Mismatches 153; Indels
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Similarity 2.0%; Pred. No. 1.72e-13;
6; Conservative 165; Mismatches 122; Indels
                                                                                                                                                                      1 (bases 1 to 7218)
Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowloox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
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166494
92724471
Sequence 14 from patent US 5670367
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1491 c 1486 g
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1491 c 1486 g
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complement(7830. .8185)
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8258. .8503
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9070. .9387
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complement(16993. .17085)
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complement(17678. .18276)
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19305. .19583
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complement(10440. .11015)
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14175. 14470
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complement(14906. 15259)
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complement(19943. .20222)
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rpt_type=tandem
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note="(A)29"
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/note="GRAIL 2 excellent exon, frame 0" complement of comp
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/rpt_family="MER20"

complement(28769. .28838)

/note="GRAIL 2 excellent exon, frame 0"

28987. .29214

/rpt_family="Alu"

/pin(29485. .29559, 29598. .29779)

/note="55% identity dbSTS:G14522 (SHGC-11312)"

29495. .29976
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3.2617. .32908
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complement(35238. .35331)
/rote="GRAIL 2 excellent exon, frame 1"
frote="GRAIL 2 excellent exon, frame 1"
frote="GR
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complement(31573. 31724)
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/rpt_unit=A
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1 (bases 1 to 215)
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 29-OCT-1996,
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Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
Location/Qualifiers
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Pred. No. 2.75e-04;
56; Mismatches 59; Indels
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complement(38069. .38215)
/note="GRAIL 2 excellent exon, frame 0"
complement(38462. .38578)
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                                                                                                      Note: remainder of annotations omitted.
                                                                                                                                                                         Query Match 1.3%;
Best Local Similarity 13.8%;
Matches 12; Conservative
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Best Local Similarity 12.9%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                  1495 GGCCTGGGGGCACCAGCCGGCAGGCCGCACGAAGCCGTACACCTGCCAGGGGC 1436
                                                                                                                                                                            126 AMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGT 185
                                                                                                                                                                                                                                     66 YNYGGNNYGAAKTHYYTHTNYSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKT 125
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 74371)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
Rojeski,H., Subrammanian,S. and Martin,C.H.
Sequencing of human chromosome 5
Unpublished
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                                                                                                                                                 6 MSSSSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSAN 65
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(bases 1 to 74371)

Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Davis, C.A., Kadher, K., Miguel, T., Pitluck, S., Pollard, M., Rojeski, H., Subramanian, S. and Martin, C.H.
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Submitted (01-M06-1998) Human Genome Center, DOE Joint Genome Submitted (01-M06-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A.
Sequence submitted by.
DOE Joint Genome Institute.
Location/Qualifiers
                                                                                                            Gaps
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                                                               Length 215;
  141 others
                                                             Score 35; DB 21; Length 215,
Pred. No. 7.37e-05;
76; Mismatches 95; Indels
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join(3246. .3410,3721. .3828)
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  56
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/db_xref="taxon:9606"
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2295. .2438
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Ricke, D.O.
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                                                             Query Match 1.2%;
Best Local Similarity 13.2%;
Matches 26; Conservative
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           note="65% & 69% protein identity GenPept:U22377"
                                                                                                                                                                                                                                                                     complement(7830, .8185)
standard_name="possible repeat"
258, .8503
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complement(9740 .9845)
rpt_family="MER42"
complement(10440 .11015)
/rpt_family="Alu"
11950 .12250
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9305. 1050.
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rpt_family="MER42"
omplement(17678. .18276)
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5327. 5602
/rpt_family"Alu"
6586. 6956
/rpt_family"Ll"
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13727. 13750
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14175. .14470
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complement(14906.
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3707. .3728
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12057. .12085
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70. .9387
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.3783. .14024
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22017. .22038
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1736. .22035
                                                                    rpt_type=tandem
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note="(CA)19"
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note="(AC)12"
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/note="GRAIL 2 excellent exon, frame 0"
39378.38741. 38995,
39071. 39205, 39532. 39630, 39935.
40561,41868. 41972,42103. 42225,42492. 42569,
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coin(29485. .29559, 29598. .29779)
'note="9584 identity dbsTs:G14522 (SHGC-11312)"
'psp55. .29976
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complement(35238 . 35331)
/note="GRAIL 2 excellent exon, frame 1"
/note="GRAIL 2 excellent exon, frame 1"
36392 . 36663
/rpt_family="Alu"
36901 . 3722
/db_xref="dbEST:Al025011"
36901 . 37164
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/note="GRAIL 2 excellent exon, frame 1"
complement(32159, 33232)
/note="GRAIL 2 excellent exon, frame 2"
32388, 32488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25712. 28930
/rpt_family="MER20"
complement(28769. 28838)
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complement(30401. .30536)
/note="GRALL 2 excellent exon, frame
complement(30682. .30733)
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3022. .23326
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32977. 33088
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complement(33670. 33785)
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?7191. .27477
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'rpt_type-tandem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"preproprotease"
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LTAQAAVRRAAADEPPEWNDFGV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                        Db 15918 KCKCTSTSKCSCMSRSKSKRGWGYRSWKKYRCAMWMTCKSSKCWCWSYRMRMKCYSCSYC 15977
                                                                                                                                                                                                         62 CSGTSGTSTCSCGSCGSCTSCTSGAGGGSGGSGCSGCSGTSCTSGGGGCCCTSGCSCTST 121
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                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces griseus
Eubacteria: Firmicutes: Actinomycetes; Streptomycetees;
Streptomycetaceae; Streptomyces.
1 (bases 1 to 201)
Garvin, R.T. and James, E.
Production of active proteins containing cystine residues
Pratent: EP 0222279-A 2 20-MAY-1987;
44379. .44507))
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/note="78%-100% protein identity GenPept:U18937"
complement(38069. .38215)
/note="GRAIL 2 excellent exon, frame 0"
complement(38462. .38578)
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Synthetic DNA for preproprotease leader & prochymosin.
A10161
9490655
                                                                                                                                  Length 74371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 201;
                                                                                                                                Score 34; DB 26; Length 743
Pred. No. 2.75e-04;
46; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 21; Length 201
Pred. No. 4.44e-02;
35; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                     A10158 201 bp DNA PAT
S.gilseus gene for preproprotease (partial).
A10158
9490196
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/organism="Streptomyces griseus"
/db_xref="taxon:1911"
1. .>201
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                                                                                                                                                                                                                                                                               2549 CACTGGACGIAGGACTIGCCCCTG 2526
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Note: remainder of annotations omitted.
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces griseus.
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Best Local Similarity 36.1%;
Matches 52; Conservative
                                                                                                                                Query Match 1.2%;
Best Local Similarity 15.5%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cangene Corporation
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                                             misc_feature
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AUTHORS
TITLE
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/product="preproprotease leader & prochymosin"
\Darxet="pi0;9490656"
/translation="MPSPVSPAESPAPQPGRPRPVVSRRLLEGGAAVLGALALSASP
LTAQAAVRRAAREITRIPLYKGK"
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synthetic construct
artificial sequence.
I (bases 1 to 201)
Garvin, R.T. and James, E.
Production of active proteins containing cystine residues
Patent: EP 0222779-A 6 20-MAY-1987;
Cangene Corporation
unclassified.
1 (bases 1 to 201)
Garvin,R.T. and James,E.
Production of active proteins containing cystine residues
Patent: EP 0222279-A 5 20-MAY-1987;
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Synthetic DNA for preproprotease leader & prochymosin.
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9489115
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Pred. No. 4.44e-02;
35; Mismatches 57; Indels
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Pred. No. 4.44e-02;
35; Mismatches 57; Indels
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1. .>201
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    .201
    /organism="synthetic cc/db_xref="taxon:32630"
    51 c 66 g

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1.1%;
Best Local Similarity 36.1%;
Matches 52; Conservative
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Best Local Similarity 36.1%;
Matches 52; Conservative
                                                                                                      Cangene Corporation
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Search completed: Fri Dec 25 12:03:06 1998 Job time : 11319 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

 $\rm n.\,a.$ - $\rm n.\,a.$ database search, using Smith-Waterman algorithm with gap extension penalties as well as gap opening penalties MPsrch_nna

Fri Dec 25 12:03:25 1998; MasPar time 8218.69 Seconds 620.553 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-951-733-13 (1-2848) from US08951733.seq (1 of 2848 Description: Perfect Score: N.A. Sequence:

1 CACGCGTCCGGGCAGCGCTG........GATGCCGGCCCACGGCCTAT 2848 GTGCGCAGGCCCGTGCCGGATA

TABLE default Gap open 30; Gap extend 1 Scoring table:

Dbase 0; Query 0 •• STD Nmatch

2275026 seqs, 895388244 bases Searched:

×

Post-processing:

Minimum Match 0% Listing first 45 summaries embl-est55 Database:

5:9b_est1 6:9b_est10 7:9b_est11 8:9b_est12 9:9b_est13 10:9b_est14 11:9b_est15 12:9b_est16 13:9b_est17 114:9b_est18 15:9b_est2 17:9b_est2 17:9b_est2 18:9b_est2 17:9b_est2 17:9b_est2 13:9b_est2 13:9b_est2 13:9b_est4 21:9b_est5 22:9b_est6 23:9b_est7 24:9b_est8 25:9b_est9 26:9b_gss1 27:9b_gss2 28:9b_gss3 29:9b_gss4 1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3 genbank-est107 Database:

Mean 11.733; Variance 2.670; scale 4.395 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ď					
Result		Query					
NO.	Score		Match Length DB	8	O O	Description	Pred. No.
-	385	13.5		8	AA281296	zt08902.rl NCI CGAP GC	0.00e+00
. 4	187	6.6	409	24	AA311750	EST182469 Jurkat T-cel	
υ υ	3 58	2.0		12	AA754459	97SN1787 Rice Immature	
4	1 54	1.9		12	AA754459	97SN1787 Rice Immature	
W1	5 49	1.7		12	AA754458	97SN1784 Rice Immature	
υ υ	5 44	1.5		12	AA754458	97SN1784 Rice Immature	
-	7 33		375	23	AA200728	mul3h09.rl Soares 2NbM	
ω	33		2275	11	AF034173	Homo sapiens ntcon2 co	
J	31		099	11	AF034177	Homo sapiens ntconf co	
7	28	1.0		12	AF038250	Homo sapiens clone ntc	
c 11	1 28		1287	12	AF038250	Homo sapiens clone ntc	
0	2 25		143	18	A1171394	EST217350 Normalized r	

13 14 15 16 17 18 19 19 19 19 10 21 22 22 23 24 24 25 26 33 27 27 27 27 27 28 29 29 29 20 31 44 44 44 44 44 44 44 44 44 4	25 0.9 181 6 AA386587 vw68hll.rl Stratagene 8.99e-04 25 0.9 213 16 R72797 vw68hll.rl Stratagene 8.99e-04 213 16 R72797 vw68hll.rl Stratagene 8.99e-04 213 16 R72797 vw68hll.rl Stratagene 8.99e-04 25 0.9 242 15 An012107 EST20558 Normalized r 8.99e-04 27 0.9 301 14 AA882818 FST191723 Normalized r 8.99e-04 27 0.9 302 15 An010844 EST205255 Normalized r 8.99e-04 27 0.9 318 14 AA79977 AND CIT-HSP 228863.FF CIT- 6.33e-06 27 0.9 318 16 H50134 vo27a07.rl Homo sapien 8.99e-04 25 0.9 318 16 H50134 vo27a07.rl Homo sapien 8.99e-04 25 0.9 318 16 H50134 vo27a07.rl Homo sapien 8.99e-04 25 0.9 359 24 AA303595 EST1605 Aorta endothe 8.99e-04 25 0.9 359 24 AA303595 EST1605 Aorta endothe 8.99e-04 25 0.9 350 19 T26788 VATA bloodstrea 7.82e-05 25 0.9 478 14 AA925372 UI-R-Al-dx a-11-0-UI-S 8.99e-04 420 17 AN071447 UI-R-Al-dx a-11-0-UI-S 8.99e-04 420 17 AN071447 UI-R-Al-dx a-11-0-UI-S 8.99e-04 25 0.9 478 14 AA925372 UI-R-Al-dx a-11-0-UI-S 8.99e-04 25 0.9 478 14 AA925372 UI-R-Al-dx a-11-0-UI-S 8.99e-04 25 0.9 478 14 AA925372 UI-R-Al-dx a-11-0-UI-S 8.99e-04 25 0.9 500 10 AA62227 UI-R-Al-dx a-11-0-UI-S 8.99e-04 25 0.9 500 10 AA62227 UI-R-Al-dx a-00-0-UI-S 8.99e-04 275 11 AR041177 UI-R-Al-dx a-00-0-UI-S 8.99e-04 25 0.9 500 10 AA62227 UI-R-Al-dx a	ALIGNMENTS AAA281296 389 bp mRNA EST 14-AUG-1997 zt08902.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5', AA281296 g1924134 mRNA sequence. AA281296 g1924134 EST 14-AUG-1997 AA281296 g1924134 human Homo sapiens EST Homo sapiens ENGARPLACE Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo. Homo: Nortchata; Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo. Nortchata; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo. Nortchata; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo. Nortchata; Mammalia: Eutheria; Primatesia was primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 385. 1. 389 /Organism="Homo sapiens" /Organism="Homo s
	11111111111111111111111111111111111111	TESULT 1 LOCUS LOCUS ACCESSION NID KEYWORDS SOURCE AUTHORS TITLE JOURNAL COMMENT SOURCE SOURCE

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1 (bases 1 to 409)

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Wenfactock,K.G., Gocayne,J.D.,
White,O., Sutton,G. Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Haddlom,E., Hinkle,P.S.J.M.,
Kelley,J.M., Kelley,J.C., Liu,L.T., Marmaros,S.M., Merrick,J.M.,
Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Sockt,J.L., Saudek,D.M., Shriley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1930 cecrrcarcecaacereacesecrecesecearreraacaresacracereceresea 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 CGCTTCATCCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCAGAACGITCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTG 360
                                                                                                                                                                                                                                                                                                                                                                                          AA311750 409 bp mRNA EST 19-APR-1997
EST182469 Jurkat T-cells VI Homo sapiens CDNA 5' end, mRNA
                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                              Length 389;
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Pred. No. 0.00e+00;
0; Mismatches 2; Indels
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Matches 387; Conservative
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He,W.W., Hu,J.S., Greene,J.W., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Melssner,P.S., Olsen,H., Raymond,L., Wei,Y.F., WingyJ., Xu,C., Yu,G.L., Ruben,S.W., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA754459 252 bp mRNA EST 20-JAN-1998 97SN1/787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1/787, mRNA sequence.
AA754459 92801165
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Bukaryotae; Viridiplantae; Charophyta/Embryophyta group;

Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;

Poales; Poaceae; Oryza.

1 (bases 1 to 252)

Mahn, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P.,

Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,

Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                     The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA rel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org Email: arkerlav@tigr.org additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
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Pred. No. 5.02e-269;
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/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
<1. .>409 133 g 86 t
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1. .409
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Similarity 98.9%;
87; Conservative
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Contact: Eun M.Y.
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/organism="oryza sativa"
/cultivar="hilyang23"
/cultivar="hilyang23"
/note="vector: paluescript SK(+); Site_1: EcoRI; Site_2:
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AA754459 92801165
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                                                                                    Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0307
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
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Submitted by Back Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
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Pred. No. 1.91e-48;
88; Mismatches 69; Indels
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National Inst. of Agri. Sci. and Tech, RDA
Wavnon, Kunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
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Best Local Similarity 12.8%;
Matches 23; Conservative
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/organism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
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Xho1; Directional cDNA library inserted into lambda ZAPII
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/dev_stage="S days after pollination"
/lab_host="E. coli Solk"
s a 21 c 12 g 35 t 179 others
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AA754458 92801164
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1 (bases 1 to 247)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.
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/cultivar="%ilyang23"
/note="Vector: PBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI: Directional cBNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3'end with Xho I site."
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel. 82 331 290 0301
Fax: 82 331 290 0307
Fax: 82 300 0307
Fax: 8
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Best Local Similarity 8.7%; Pred. No. 2.26e-42;
Matches 18; Conservative 105; Mismatches 85; Indels
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Location/Qualifiers
1. .252
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/organism="Oryza sativa"
/organism="Oryza sativa"
/cultivar="Milyang23"
/rote="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note="Vector: DBluescript SK(+); Site_1: EcoRI; Site_2:
//orca to fond with EcoRI and 3' end with Xho I site."
/db_xref="taxon.4530"
/clone="97SN1784"
/clone="97SN1784"
/clone="197SN1784"
/clone="197
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AA754458 92801164
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Bukaryotea, Viridiplantae; Charophyta/Embryophyta group;

Embryophyta; Tracheophyta; seed plants; Magnollophyta; Liliopsida;

Poales; Poaceae; Oryza.

I (basea: 1 to 247)

Nahm, B. H., Kim, J. K., Cheong, J. J., Kim, S. I., Hahn, T. R., Moon, E. P., Kim, W. T., Kim, W. Y., Yang, M. S., Park, R. D., Sohn, U. I., Kang, K. Y., Lee, M. C. and Eun, M. Y.

Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
/db_xref="taxon:4530"
/clone="978N1784"
/clone="978N1784"
/clone=lib="#xice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/lab_host="E. 21 g 34 t 169 others
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Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido. Korea
Tel: 82 331 290 0307
Fax: 82 331 290 0307
Fax: 82 bmail: myeun6sun20.asti.re.kr
Submilt: myeun6sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongih, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 TNTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBTAYCDYBHYBDRANHVDDTRCTNDRGYC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 CCTGGGACGCACGGCCCCCCCCCCCCTCCTTCCGCCAGGTGTCCTGCTGAAGG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 NYTASDNGTSATKRVTGYDKTDSDCGGGCWRKVTYGSSBYBRCGVNVMVRTTSMWTDKST 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 AGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGGCGGCGCGCGAAGAACGTGCTGCCT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                          28 TBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDNAHCRYTVBWYYARSKYGYGTBYYSWNVD 87
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                                                                                                                                                                                                                                                                                                             Length 247;
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Pred. No. 5.98e-35;
93; Mismatches 88; Indels
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Best Local Similarity 13.0%;
Matches 27; Conservative
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(bases 1 to 375)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286
                                                                                                                                                                                                                                                                                 2133 GGCCCTGTGGATATCGTCCAGGCCCAGCACAGAGGCGCCCAGGAGGCCGGGGCGCCGGGCCCGCGCCCAGAAAA
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                          111 SNSVVYVWBTAYCDYBHYBDRANHVDDTRCTNDRGYCNYTASDNGTSATKRVTGYDKTDS 170
                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                171 DCGGGCWRKVTYGSSBYBRCGVNVMVRTTSMWTDKSTKMBSMDMSRRSRV 220
         Length 247;
         Score 44; DB 12; Length 247
Pred. No. 9.37e-28;
60; Mismatches 36; Indels
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High quality sequence stop: 361.
Location/Qualifiers
1.375
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/sex="male"
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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/dev_stage="4 weeks"
/lab_nost="DH10B"
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a 95 c 105 g
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Query Match 1.5%;
Best Local Similarity 12.7%;
Matches 14; Conservative
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                                                                                     REFERENCE
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Homo sapiens ntcon2 contig mRNA, partial sequence, mRNA sequence.
AF034173
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Homo sapiens ntcon6 contig mRNA, partial sequence, mRNA sequence.
AF034177
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L Unpublished
L Unpublished
L Chases 1 to 2275)
RS Tripodis, N. and Ragoussis, J.
Direct Submission
NAL Submitted (13-NOV-1997) Division of Medical and Molecular General Submitted (13-NOV-1997) Division of Medical Submitted (13-NOV-1997) Division of Medic
                                                                                                            144 AGAGCATCTCTATGAATGAGCAGCAGCAGCCTGTTTGACTTCTTCCTGCACTTCCTGC 203
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1 (bases 1 to 660)
Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Bukaryotae; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria;
Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2275)
Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
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  Length 375;
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Score 33; DB 23; Length 375
Pred. No. 5.05e-13;
0; Mismatches 16; Indels
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/clone="ntcon2 contig"
/tissue_type="liver; brain"
/dev_stage="fetus"
/note="similar to Br140"
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Query Match 1.2%;
Best Local Similarity 75.4%;
Matches 49; Conservative
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Best Local Similarity 13.3%;
Matches 11; Conservative
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Homo sapiens
Eukaryotes, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryotes, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryotes, Actarrhini; Hominidae; Homo.
1 (bases 1 to 1287)
Tripodis,N. and Ragoussis,J.
Direct Submission.
Submission.
Submitted (12-DEC-1997) Division of Medical and Molecular Genetics,
Guy's Hospital, 7th floor, Guy's Tower, London SE1 9RT, UK
Location/Qualifiers
                                    boundary
Unpublished
Unpublished
2 (bases 1 to 660)
2 Tripodis,N. and Ragoussis,J.
Tripodis,N. and Ragoussis,J.
Direct Submitsed (13-NoV-1997) Division of Medical and Molecular Genetics,
Submitted (13-NoV-1997) Division of Medical and Molecular Genetics,
Guy's Hospital, 7th floor, Guy's Tower, London SEl 9RT, UK
Location/Qualifiers
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Homo sapiens clone ntcon9 mRNA, partial sequence, mRNA sequence.
AF038250
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centromeric to human MHC across the \mathsf{6p21.2}\text{-}\mathsf{6p21.3} chromosomal boundary
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Pred. No. 1.45e-10;
31; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 12;
Pred. No. 4.79e-07;
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/dev_stage="fetal"
/tissue_type="brain; liver"
/note="similar to HSRP20"
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                                                                                                                                                                                                                     1. .660
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
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/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
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/tissue_type="fetal bra
/note="similar to CutA"
161 c 173 g 1
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Best Local Similarity 15.6%;
Matches 7; Conservative
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Best Local Similarity 29.1%;
Matches 23; Conservative
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                                                                                             Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 1287)

Tripodis,N. and Ragoussis,J.

Direct Submission

Submitted (12-DEC-1997) Division of Medical and Molecular Genetics,
Guy's Hospital, 7th floor, Guy's Tower, London SE1 9RT, UK

Location/Qualifiers
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1 (bases 1 to 143)
1 (Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
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/note="Organ: muscle; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
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                                                                  Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1287;
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Pred. No. 4.79e-07;
29; Mismatches 19; Indels
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/note="similar to HSRP20"
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/db_xref="taxon:9606"
/chromosome="6"
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/clone="ntcon9"
/dev_stage="fetal"
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Best Local Similarity 23.8%;
Matches 15; Conservative
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Other_ESTs: TC52270
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Rattus sp.
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N.H., Rirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Flizgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblow, E., Hinkle, P.S., Jr.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Naquyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P.S., Olsen, H.,

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fannon, R., Rosen, C.A., Haseltine, M.A., Fields, C.,

Fraser, C.M., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.hfml)
Seq primer: MI3 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                          AA386387 181 bp mRNA EST 22-APR-1997 EST81369 Prostate gland I Homo sapiens cDNA 5' end similar to prolyl 4-hydroxylase, beta subunit/protein disulfide isomerase/thyroid hormone-binding protein, mRNA sequence.
                                                                     Gaps
                                                                  ;
0
Score 25; DB 18; Length 143; Pred. No. 8.99e-04; 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 others
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                                                                                                                                                                  103 GGGAGCGCACGGCTCGGCAGCGGGGACGCGCGCGCGCGTG 57
                                                                                                                                 4 GGGAGCGCATGGGCCCGCTGCGGGGCTCGCGCCGCCGCTGGTG
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   Query Match 0.9%;
Best Local Similarity 76.6%;
Matches 36; Conservative
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Bouterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 213)
Hillier, Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Final: est@watson.wustl.edu
High quality sequence stops: 185
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 CIGCCGCIGCCCACGTICGIGCGCCCCGAGGCCTGGCGCTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 CIGCCCCGGGCCACGTITGIGAGCAGCGTGAGACCCCGAGAGCTCTCGGCTG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25; DB 16; Length 213; Pred. No. 8.99e-04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: Fri Dec 25 14:50:06 1998 Job time: 10001 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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The WashU-Merck EST Project
Unpublished (1995)
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72 C
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Best Local Similarity 74.5%;
Matches 38; Conservative
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9846829
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ORIGIN
                                                                                                                                                                                                                                                                                    ORGANISM
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JOURNAL
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AUTHORS
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                                                                                                                                                                                          AA855630 187 bp mRNA EST 06-MAR-1998 vw68h11.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone 1260165 5' similar to TR:Q99960 Q99960 PLAKOPHILIN 2A. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryota, Metazoa (Chordata; Vertebrata; Mus.
1 (bases 1 to 187)
Marra M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton bark Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 286 1810
Fax: 315 286 1810
Fax: 316 286 2800 wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="NHSWiss"
/strain="NHSWiss"
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
BCORI; Site_2: Xhof; Cloned unidirectionally. Primer:
Oligo dT. 93 pooled NH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5
adaptor sequence: 5' GAATTCGGACGAG 3' ~3' adaptor
/db_xref="taxon:10090"
/clone="1260165"
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                    Gaps
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/lab_host="SOLR (kanamycin resistant)"
65 c 70 g 23 t
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Pred. No. 8.99e-04;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:66217
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 178.
Location/Qualifiers
1..187
/organism-"Mus musculus"
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Pred. No. 8.99e-04;
0; Mismatches 5
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The WashU-HHMI Mouse EST Project
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Best Local Similarity 85.7%;
Matches 30; Conservative
Best Local Similarity 70.0%;
Matches 42; Conservative
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                                                                                                                                                                                                                                                                                                                                                    house mouse.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

 $\rm n.a.~~i.a.$ database search, using Smith-Waterman algorithm with gap extension penalties as well as gap opening penalties MPsrch_nna

Fri Dec 25 14:50:27 1998; MasPar time 906.76 Seconds 427.322 Million cell updates/sec Run on:

Tabular output not generated.

1 CACGCGTCCGGGCACCCTG........GATGCCGGCCCACGGCCTAT 2848 GTGCGCAGGCCCGTGCGGATA. >US-08-951-733-13 (1-2848) from US08951733.seq (1 of 2848 Title: Description: Perfect Score: N.A. Sequence:

TABLE default Gap open 30; Gap extend 1 Scoring table:

188442 segs, 68026449 bases x 2 Dbase 0; Query 0 STD Searched:

Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

i.partl 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part10 11:part11 18:part18 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 39:part39 33:part31 32:part31 33:part31 33:part31 33:part31 33:part31 33:part30 40:part40 n-geneseq32 Database:

Variance 6.270; scale 1.551 Mean 9.722; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Query Pred. No. 45 1.6 91 9 Q51746 Oligonucleotide probe 1.95e-10 45 1.6 91 9 Q51746 Oligonucleotide probe 1.95e-10 40 1.4 114 12 070466 Generic DNA sequence 2.32e-09 39 1.4 114 12 070469 Generic DNA sequence 2.97e-07 41 1.4 18 32 776405 Human endothelin-1 an 2.97e-07 41 1.4 18 18 1164 Base substituted E.co 2.97e-07 41 1.4 12 070468 Generic DNA sequence 9.79e-07 38 1.3 114 12 070466 Generic DNA sequence 9.79e-07 36 1.3 114 12 070467 Generic DNA sequence 1.03e-05 36 1.3 114 12 070467 Generic DNA sequence 1.03e-05 36 1.3 114 12 070466			æ					
91 9 051746 Oligonuclectide probe 91 9 051746 Oligonuclectide probe 204 1 N81164 Base substituted E.co 114 12 070466 Generic DNA sequence 178 32 776405 Human endothelin-1 an 204 1 N81164 Base substituted E.co 114 12 070468 Generic DNA sequence 114 12 070465 Generic DNA sequence 114 12 070467 Generic DNA sequence	Š	Score	Query Match	Length I	99		Description	Pred. No.
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204 1 N81164 Basé substituted E.co 114 12 070466 Generic DNA sequence 178 32 776405 Human endothelin-1 an 204 1 N81164 Base substituted E.co 114 12 070468 Generic DNA sequence 114 12 070467 Generic DNA sequence		45	1.6	91	6	051746	Oligonucleotide probe	1.95e-10
14 12 070466 Generic DNA sequence 14 12 070469 Generic DNA sequence 178 32 776405 Human endothelin-1 an 204 1 N81164 Base substituted E.co 114 12 070468 Generic DNA sequence 114 12 070467 Generic DNA sequence 114 12 070470 Generic DNA sequence 114 12 070465 Generic DNA sequence 114 070465 Generic DNA sequence 070465		43	1.5	204	-4	N81164	Base substituted E.co	2.32e-09
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						ALIGNMENTS				
RESULT	ULT 1	_								
ΩĮ	051746	5 standard	lard;	CDNA;	91	BP.				
AC	051746	;;								
Ę	31-MAY	7-1994	(first		entry)					
DE	Oligor	ncleot	ø	٠.	MK14-A	-A				
ΚW	Oligonucleotid	ncleot	ö	DNA p	probe	; mycobacteria;	ria; disease diagnosi	18;		
ΚW	ss.									
SO		O								
PN	EP-571911									
PD		3-1993.								
ç		9	,	100						

Samples Claim 3: Page 14; 23pp; English. Claim 3: Page 14; 23pp; English Coligonucleotide probe MK14. Coligonucleotide probe MK14. Claim 20: Claim 3: Claim 2: Claim 3: Claim 24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT) BECTON DICKINSON CO.
Shank DD, Sears PA;
WPI; 93-378844/48.
New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria acid in

Gaps ö 5; Indels Query Match 1.6%; Score 45; DB 9; L. Best Local Similarity 7.3%; Pred. No. 1.95e-10; Matches 4; Conservative 46; Mismatches 5 염

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Length 91;

390

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Best Local Similarity 20.9%;
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Introducing random point mutations into nucleic acods -

by prepn of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.

Disclosure; p; English.

Random point mutations were introduced into the alpha fragment of
E.coli beta galactorsidase. The wild type sequence was obtained as a
Single stranded template and an oligonucleotide was hybridised to
it to generate a popn of DNA molecules which terminate at all
possible nucleotide positions within a specified region. The
variable 3' ends generated in this way are used as primers for
reverse transcriptase. Nucleotides are misincorporated by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 tccggcgssvhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvhhvhyhvyvsvct 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                            MK14
but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 Others;
                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide probe MK14.A consists of nucleotides 5-95 of 0(051735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 051735-45 and 051747-59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T; WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                               nseq
                                    31-WAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                      New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 9; Length 91;
Pred. No. 1.95e-10;
45; Mismatches 7; Indels
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  BP.
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Local Similarity 11.9%;
les 7; Conservative
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standard; cDNA; 91
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26-MAY-1992; US-889651
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30-MAR-1988; 105163.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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051746
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DB 1; Length 204;

Score 43;

1.5%;

Query Match

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Terbulk Roble.

Terbulk Roble.
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                                                                                                                      bcyrraggnyccccggggywccgagcycgaayycdchvgccgymrttthhyrrmrbnvyrd 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generic DNA sequence to generate a random TSAR-9 petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                          Gaps
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Pred. No. 8.94e-08;
32; Mismatches 70; Indels
Pred. No. 2.32e-09;
57; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "this sequence represents 'Z'; Z sequence of 6, 9 or 12 nucleotides (see comments)"
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m I}
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FFOW/RES DM, RAV RY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4%;
llarity 8.9%;
Conservative
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Matches 10; Conser
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P-PSDB; R65152.
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01-FEB-1994;
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(first entry) standard; DNA; 178

15-SEP-1997

T76405;

LT 6

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PF Fowlkes DM, Kay BK;

WHI: 94-279739/34.

PT Fowlkes DM, Kay BK;

PT I Gentifying proteins or peptide(s) which bind a ligand - by

Identifying proteins or peptide(s) which bind a ligand - by

Screening a recombinant vector library expressing fusion proteins

comprising a binding domain and an effector domain

PS comprising a binding domain and an effector domain

Disclosure; Page 35; 255pp; English.

CTALS generic formula can be represented as follows: XTGC)(NNB)10-

CTCC)(NNB)5Z(NNB)2TGC)(NNB)14(TGC)Y. X and Y are flanking restriction

Sites (X is not the same as Y) that are not specified further. This

Sequence generates peptides that are cloverleaf in structure. Other

CC generated by these generic sequences are shown in R65150-54. Takks are

CC generated by these generic sequences are shown in R65150-54. Takks are

CC generated by these generic sequences are shown in R65150-54. Takks are

CC generated by these generic sequences are shown in R65100-54. Takks are

CC generated by these generic sequences are shown in R65100-54. Takks are

CC generated by these generic sequences are shown in R65100-54. Takks are

CC generated by these generic sequences are shown in R65100-54. Takks are

CC concatenated heterofunctional proteins or peptides, comprising at least

CC contains I sold the perides or hat it is expressed peptide

CC contournerional rigidity to the peptides. These residues confer some degree of

CC conformational rigidity to the peptides. The TSARs or compass. Comprising

CC conformational rigidity to the peptides. The TSARs or compass.

CC conformational rigidity to the peptides. The TSARs or compass.

CC conformation of macromolecules, eg. monoclonal or polyclonal antibodies

CC conformation or in vivo antibody production. The TSARs are easily

CC characterised and have designed activity allowing direct and rapid

CC characterised and have designed activity allowing direct and rapid
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149 recedence creases and reconstance and reco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generic DNA sequence to generate a random TSAR peptide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                            bnnbnnbnnbnnbnnbnnbhnbtgcnnbnnbnnbnnbnnbnnbnnbnnb 114
                                                                                                                                                                                                              208 CGCGCGCTGGTGGCCCAGTGCCTGGTGCGTGCCTGGGACGCACGGCCGC 259
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sequence of 6,9 or 12 nucleotides (see
comments)"
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                                                                                                                                                                                                                                                                                                                      .r 5
Q70469 standard; DNA; 114 BP.
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(UYNC-) UNIV NORTH CAROLINA.
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Sequence 114 BP; 0 A
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US-176500.
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Matches 8; Conser
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31-JAN-1994;
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A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonucleotide specific for the human endothelin-1, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-reactive airways. Sequence 178 BP; 0 A; 52 C; 46 G; 32 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening. Disclosure; p; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NoV-1990 (first entry) assess alpha-fragment. Base substituted E.coli beta-galactosidase alpha-fragment; base substitutions; ss. Escherichia coll.
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                                                                                         Human endothelin-1 antisense oligonucleotide.
Asthma; airway epithelium; adenosine free; cystic fibrosis;
chronic obstructive pulmonary disease; bronchitis; ss.
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Pred. No. 2.97e-07;
34; Mismatches 17; Indels
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187..204
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Metzger WJ, Nyce JW;
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                                                                                                                                                                                                                                                           19-DEC-1996.
06-JUN-1996; U09306.
07-JUN-1995; US-474497.
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                                                                                                                                                                                                 Synthetic.
WO9640162-Al.
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Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins
FT comprising a binding domain and an effector domain
Disclosure; Page 35; 255pp; English.

Comprising a binding domain and an effector domain
Disclosure; Page 35; 255pp; English.

COV468 is a generic DNA sequence used to generate random TSAR (Totally COV468 is a generic DNA sequence used to generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)7(TGC)(NNB)10Y. X

COMPRISION TO THE SATIATION SILES (X is not the same as Y) that are not specific peptides generated by these generic sequences are shown in COVAET Specific peptides generated by these generic sequences are shown in CR6151-54. TSARS are concatenated beterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with a light for a light and and a second effector peptide portion that is chanically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed conferses of peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confers some degree of conformational rigidity to the peptides. The TSARS or comprise a live to the peptides.
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                                                                                                                                                                                                                                                                                                                                                              2093 AGGAGGCGGGGGCGCGCCGCTGTAGTTGAGCACGTGAACAGTGCCTTCACCCTC 2034
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                                                                                                                                                                                                                                                                                                                                        50 aggnyccccgggywccgagcycgaayycdchvgccgymrttthhyrrmrbnvyrdynrsd 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
single stranded template and an oligonucleotide was hybridised to it to generate a popp of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which see also P80575.
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/note= "this sequence represents 'Z'; Z can be a
sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                 108 Others;
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                                                                                                                                                                                                                                                        Score 41; DB 1; Length 204;
Pred. No. 2.67e-08;
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                                                                                                                                                                                                                                                                                                 58; Mismatches
                                                                                                                                                                                                              17 G;
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Q70468 standard; DNA; 114 BP
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UNNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                          1.48;
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                                                                                                                                                                                                                                                                                                 27; Conservative
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/*tag=
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P-PSDB; R65154.
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05-APR-1995
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deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal artibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
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                                                                                                                                                           151 CGGCGCCTGGGGCCCCAGGGCTGGCGGTGGTGCAGCGCGGGGGACCCGGCGGCTTTCCGC 210
                                                                                                                                      Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                             Score 38; DB 12; I
Pred. No. 9.79e-07;
34; Mismatches 73;
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Q70465 standard; DNA; 114 BP.
Q70465;
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/note= "this
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(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Kay BK;
                                                                                             Query Match 1.3%;
Best Local Similarity 4.5%;
Matches 5; Conservative
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P-PSDB; R65150 and R65151.
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US-176500.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins promprising a brinding domain and an effector domain bisclosure; Page 35; 255pp; English.

Disclosure; Page 35; 255pp; English.

Comprising a brinding domain and an effector domain bisclosure, Page 35; 255pp; English.

Comprising a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reasperts) peptides. This generic formula can also be represented as follows: X(NNB)16(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)12(TGC)(TNB)1
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                                                                                                                                      2490 CTTCCTACGCTTCATGTGCCACCACGCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG 2549
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                                      Length 114;
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Pred. No. 1.03e-05;
34; Mismatches 74; Indels
                                  Score 38; DB 12; Length 114
Pred. No. 9.79e-07;
33; Mismatches 73; Indels
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sequence of 6, 9 or 12 nucleotides (see
comments)"
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2 G;
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Q70467 standard; DNA; 114 BP.
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/note= "this
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(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Ray BK;
WPI; 94-279739/34.
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Local Similarity 3.6%;
hes 4; Conservative
                                                   larity 5.4%;
Conservative
 0 A;
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 114 BP;
                                                    Sest Local Similarity
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P-PSDB;
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Forecasting a recombinant vector library expressing fusion proteins

Forecasting a binding domain and an effector domain

Disclosure; Page 36: 255pp; English.

O70470 is a generic DNA Sequence used to generate random TSAR (Totally

O70470 is a generic DNA Sequence used to generate random TSAR (Totally

CACACIANDS) English.

CACACIANDS (ACACIANDS) (ACAC
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10-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR, totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                  Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion pro
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/note= "encoded by Z (see comments)"
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKS DM, KAY BK;
WPI: 94-279739/34.
P-PSDB; RS8378.
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Q70470 standard; DNA; 114 BP.
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PT Identifying proteins or peptide(s) which bind a ligand - by

Screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure; Page 35; 255pp; English.

COT0465 is a generic DNA Sequence used to generate random TSAR (Totally

COT0465 is a generic DNA Sequence used to generate random TSAR (Totally

COT0465 is a generic DNA Sequence used to generic formula can also be

COT0465 is a generic DNA Sequence used to generic sequences are shown in COT0465 is and Y are flanking restriction Sites (X is not the same as Y) that are

COT0465 is a generic OT0465 generic sequences are shown in COT0465 generic sequences are shown in GENERIC SECTOR SE
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Generic DNA sequence to generate a random TSAR petide library. TSAR: totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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sequence of 6, 9 or 12 nucleotides (see
comments)"
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Pred. No. 9.79e-07;
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Q70468 standard; DNA; 114 BP.
Q70468;
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31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
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larity 4.5%;
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Best Local Similarity
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Synthetic Affinity Reagents) peptides. This generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)62(NNB)7(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic Sequences are shown in Q70466-68. Cother specific peptides generated by these generic sequences are shown in R8515-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or compens. comprising a TSAK binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal artibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.

Sequence 114 BP; 0 A; 2 C; 2 C; 2 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure, Page 35; 255pp; English.
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comments of 6, 9 or 12 nucleotides (see
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                                                                          or 12 nucleotides (see
/*tag= a
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^~~nence of 6, 9 or 12 nucleotide
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Pred. No. 9.79e-07;
34; Mismatches 73;
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKS DW, KAY BK;
WPI: 94-279739/34.
P-PSDB: R65154.
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Q70467 standard; DNA; 114 BP.
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01-FEB-1994; U00977.
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Discussure; regges 35, 203Pp; language.

Confering a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)16(TGC)(NNB)16(TGC)(NNB)1x. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.

Confer specific peptides generated by these generic sequences are shown in R5151-54. TSARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is comprised between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confers some degree of conformational rigidity to the peptides. The TSARs or comprise a chemically or biologically active moiety, eg. metal ion, and or in peptide, toxin or enzyme, to the specific target or on the composition or peptide, toxin or enzyme, to the specific target or on the complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
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Pred. No. 9.79e-07;
34; Mismatches 73; Indels 0; Gaps
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TSAR: totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                     Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure, Page 35; 255pp; English.
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/note= "encoded by Z (see comments)"
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Q70470 standard; DNA; 114 BP.
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31-JAN-1994; US-189331.
(UYNC-) UIIV NORTH CAROLINA.
FEWIKES DM. RAY BK;
WPI: 94-279739/34.
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Fowlkes DM, Kay BK;
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Best Local Similarity
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P-PSDB; R65152
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Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

R58378

P-PSDB;

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comprising a binding domain and an effector domain

Disclosure; Page 36; 255pp; English.

Disclosure; Page 36; 255pp; English.

Disclosure; Page 36; 255pp; English.

O'0470 is a generic DNA Sequence used to generate random TSAR (Totally Synthetic Affinity Reagens's personned as follows: X(NNB)4(CAC)(NNB)4CAC)(NNB)8Z(NNB)6CAC)(NNB)8Z(NNB)6CAC)(NNB)8Z(NNB)6CAC)(NNB)8Z(NNB)6CAC)(NNB)8Z(NNB)6CAC)(NNB)8Z(NNB)6CAC)(NNB)8Z(NNB)6CAC)(NNB)8Z(NNB)6CAC)(NNB)8Z(NNB)6CAC)(NNB)8Z(NNB)6CAC)(NNB)8Z(NNB)6CAC)(NNB)8Z(NNB)6CAC)(NNB)8Z(NNB)6CAC)(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)8Z(NNB)Z(NNB)Z(NNB)8Z(NNB)Z(NNB)Z(NNB)Z(NNB)Z(NNB)Z(NNB)Z(NNB)Z(NNB)Z(NNB)Z
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30; Mismatches 66; Indels
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Search completed: Fri Dec 25 15:11:06 1998 Job time : 1239 secs.

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RESULT
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                                                                                                                                                 \text{n.a.} - \text{n.a.} database search, using Smith-Waterman algorithm with gap extension penalties as well as gap opening penalties
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                                                                   Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd
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APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: NOVEL GENES ENCODING TELOMERASE PROTEINS
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                           sequence 52, Applicati
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
TELING DATE: 16-OCT-1997
CLASSIFICATION NUMBER: 08/08/951,733
FILING DATE: 16-OCT-1997
PRIOR APPLICATION NUMBER: 08/08/32,039
FILING DATE: 11-JUN-1997
PRIOR APPLICATION NUMBER: 08/08/32,189
FILING DATE: 11-JUN-1997
PRIOR APPLICATION NUMBER: 08/08/351,189
FILING DATE: 15-NOV-1996
ATTONNEY/AGERT INPORMATION:
NAME: 0.168541, Nancy 4,688
REGISTRATION NUMBER: 34,688
RESERENCE/POCKET NUMBER: 34,688
TELEGORMUNICATION NUMBER: A-433B
TELECOMMUNICATION INFORMATION:
TELEBHONE: (805) 447-6504
                                                                      Sequence
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US-08-617-
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STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
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MEDIUM TYPE: Floppy disk
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0; Mismatches 0;
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TELEFAX: (805) 499-8011
INFORMATION FOR SEQ ID NO: 13:
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           SEQUENCE CHARACTERISTICS:
LENGTH: 2848 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
EQUENCE 2848 BP; 437 A; 978 C;
                                                              Match 100.0%;
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                                              GTGGGCCGCCAGCACCACGCGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGAC
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                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2848; DB 22;
Pred. No. 0.00e+00;
0; Mismatches 0;
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APPLICATION NUMBER: US 08/873,039
FILING DATE: 11-UUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,189
FILING DATE: 15-NO-1996
ATTORNEY AGENT INFORMATION
NAME: 01eski, Nancy A.
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/951,733
FILING DATE: 16-OCT-1997
CLASSIFICATION: 435
    : Amgen Inc.
One Amgen Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: A-43:
TELECOMMUNICATION INFORMATION:
TELEPHOR: (805) 447-6504
TELEFAX: (805) 499-8011
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 34,688
                                                                                                   ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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nucleic acid
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Best Local Similarity 100.0%;
Matches 2848; Conservative
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                                          Thousand Oaks
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STREET: On
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                                                                                   Sequence 19, Application US/08951733
Sequence 19, Application US/08951733
Sequence 19, Application US/08951733
SENERAL INFORMATION:
APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: NOVEL GENES ENCODING TELOMERASE PROTEINS NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
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US-08-951-733-19 STANDARD; DNA; UNC; 3798
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	CCAGGGGTT	CAGGG	TTCCTGCAC	ACGGAGACC	CGGAGAC	TTGCAAAGC	TGCAAAG	SCAGAGGT 	CCCCAA	ATCCCCAAG	193	21.15	GIGCICAACI	GCTC	GACGATATC	CGATAT	GCT	CTGAGCT	\circ	GGCTCAC	TATGCCGTG	reccer	CTA	ACCIT	AGCCCGCTG	GCCCGCT	GCCTCTT	- 51 - 51	ACGT	CCTA	CTA	TGTGC	CTGCGTTTG
CCAAGCTCT	GCAGGAGC	GCAGGAGC	TGGCCAAG TGGCCAAG	TTTATGTC	TTTATGTC	GGAGCAAG	GGAGCAAG	TGTCGGAA TGTCGGAA	тссесттс	TCCGCTTC	GAGCCAGAA	AGCCAGA	CTGTTCAGC	GTTCAGC	TGGGCCTG	тесессте	ACCCGCCG	ACCCGCCG	CCCAGGAC	CCCAGGAC	TGCGTCGG	TGCGTCGG	GCCACGTC	GCCACGIC	AGGAGACC	AGGAGACC	CCAGCAGT	CCAGCAGT	GGGGCAAG	GGGCCAAG	TCTGCAGC	CTGCAGC	GGCTGCTC
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1561	1622	1621	1682	1742	1741	80	80	1862	1922	1921	86	χ. X	04	2041	2102	2101	16	2161	22	2221	28	2281	34	2341	40	2401	2462	2461	2522	2521	2582	2581	2642
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2641 CGGGACGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACC 2700
                  APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Nakanura, Toru
APPLICANT: Chapman, Raren B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Milliam
APPLICANT: Andrews, William
APPLICANT: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IS POPPY DISK
COMPUTER: IS POPPY DISK
COMPUTER: IS POPPY DISK
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,312
FILLNG DATE: 14-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
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US-08-911-312-1 STANDARD; DNA; UNC; 7029
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
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FILING DATE: 14-AUG-1997
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                                                                                                      2822 TITGITCAGAIGCCGGCCCACGGCCTAI 2849
                                                                                                                 2821 TIGITICAGATGCCGGCCCACGCCTAT 2848
                                                                                                                                                                                                   Sequence 1, Application US/08911312
Sequence 1, Application US/08911312
GENERAL INFORMATION:
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REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 782..4177
OTHER INFORMATION: /product= "human telomerase reverse of the tronsmartion transcriptase (hTRT)"
OTHER INFORMATION: /note= "CDNA contained in plasmid OTHER INFORMATION: pGRN121"
SEQUENCE 7029 BP; 1416 A; 2122 C; 2051 G; 1440 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                        Length 7029;
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Pred. No. 0.00e+00;
0; Mismatches 3; Indels
INTERPRAY: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
. TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity 99.9%;
Matches 2843; Conservative
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2757 2042 2102 2162 2222 2997 2342 2642 3477 2762 2697 2817 2877 2937 2282 3057 3117 2402 3177 3237 2522 3297 2582 3357 2702 2822 CAGACTCCGCTTCATCCCCAAGCCTGAGGGCTGCGGCCGATTGTGAACATGGACTACGT CATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCGGAACACGTA CTGCGTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTT CATCAGGGCAAGTCCTACGTCCAGGGGGATCCGCAGGGCTCCATCTCTCCAC TGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCG GCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCG CGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAA GGCACTGTTCAGCGTGCTCAACTACGAGCGGGGGGGGGCGCCCCGGCCTCGGGCGCCTC CCAGGACCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACAC ВР TGTTCAGATGCCGGCCCACGGCCTAT STANDARD; RESULT 4 ID US-08-854-050-224

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1032 CCCGGTGTACGCCGAGAGCACTTCCTCTACTACTCCTCAGGCGACAAGGAGCAGCTGCG 1091
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                                                                                                                                      132 GCCGCTGGCCACGTTCGTGCGCCCTGGGGCCCCAGGCTGGCGGCTGGTGGAGCGCGG
                                                                                                                                                                                             GGACCCGGCGCCTTTCCGCGCGCTGGTGCCCTGGTGTGTGCGTGCCCTGGGACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                852 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGTGTCACCTGCCAGACCCGCCGAAGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGGGCACCCCGGGATGCC
                                                               252 ACGGCCCCCCCCCCCCCCCCCTCCTTCCGCCAGGTGTCCTGCTGAAGGAGCTGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 961 GCACCACGCGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGGACACGCCTTGTCC
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                                           CCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC
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transcriptase (hTRT) catalytic protein
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Pred. No. 0.00e+00;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: component"
SEQUENCE 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                   Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                 STREET: Two Embarcadero Center, 8th Floor
                                                 APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Makamira, Toru
APPLICANT: Makamira, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Marley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Novel Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                            United States of America
Sequence 224, Application US/08854050 Sequence 224, Application US/08854050 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.6%;
Best Local Similarity 100.0%;
Matches 2837; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 56.
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                                                                                                                                                                                                                                                                                                          STATE:
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1020

1092 GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA 1151

GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA

1081

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US-08-912-951-1
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                                                                     AGCCGGTGTCTGTGCCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCCGAGGAGGAGGA
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATAL
TITLE OF INVENTION: HUMAN TELOMERASE CATAL
TITLE OF INVENTION: HUMAN TELOMERASE CATAL
TITLE OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: TWO Embarcadero Center, 8th Floo
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1, Application US/08912951
INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-
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OTHER INFORMATION: /product= "htrr"
OTHER INFORMATION: /note= "human telomerase revers:
OTHER INFORMATION: transcriptuse (hTRT) catalytic other INFORMATION: component"
SEQUENCE 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 OTHER.
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2837; DB 22;
Pred. No. 0.00e+00;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    015389-002600US
                                                                                                                                                      APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                      US 08/724,643
                          APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01531
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08 FILLING DATE: 01-0CT-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                       FILING DATE: 25-APR-1997
                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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337; Conservative
                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                      CGGCTTCGTGCGGGCCTGCCTGCCCGGCTGGTCCCCCCAGGCCTCTGGGGGCTCCAGGCA
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Reverse Transcriptase
CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T: Two Embarcadero Center, Eighth Floor San Francisco California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LACANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TILLE OF INVENTION: Antisense Compositions for TILLE OF INVENTION: Inhibiting Telomerase Rev NUMBER OF SEQUENCES:
ADDRESSE: TOWNSOLD: STREFT:
ADDRESSE: TOWNSOLD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compositions
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FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4015
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FILING DATE: 31-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATION NUMBER: US 08/851,843
DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09052919
Sequence 1, Application US/09052919
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-052-919-1 STANDARD; DNA; UNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                            2848
                                                                                                                                                                                                                                                                                                                                                                                                     GCCGGCCCACGGCCTAT 2837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-MAY-PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /product= "human telomerase reverse OTHER INFORMATION: transcriptase (hTRT)" SEQUENCE 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2837; DB 24;
Pred. No. 0.00e+00;
0; Mismatches 0;
                                                                                                                                              APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17685
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
APPLICATION NUMBER: WO PCT/US97/17885
APPLICATION NUMBER: WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                        015389-003600US
                         APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-A0C-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-A0C-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 01538
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415,576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs.
                                                                                                                       FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
                                                                                                                                                                                                                                                                                                                          NAME: Parent, Annette REGISTRATION NUMBER: 4
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Similarity 100.0%;
FILING DATE: 09-MAY-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 2837;
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                     CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT
                                                   GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGGTGGCACGGCTTTTGTTCAGAT
                                         GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAAC
                                                                                  CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: TELOPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: TELOPY disk
COMPUTER: TELOPY disk
COMPUTER: TEL PC COMPATIBLE
COMPUTER: TEL PC COMPATIBLE
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,981
FILING DATE: 20-FEB-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/064,322
FILING DATE: 30-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,762
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 60/054,549
FILING DATE: 11-AUG-1997
PRIOR APPLICATION NUMBER: US 60/054,549
FILING DATE: 01-AUG-1997
PRIOR APPLICATION NUMBER: US 60/047,151
FILING DATE: 20-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/047,151
FILING DATE: 20-MAY-1997
PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: WH197-11p4AM
TELEPOMMUNICATION INFORMATION:
TELEPON E: 781-861-6240
TELEPAX: 781-861-6540
FORMATION FOR CF.
                                                                                                                                                                                                                                US-09-026-981-35 STANDARD; DNA; UNC; 4023
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                                                                                                                                                                                                                                                                                             APPLICANT: Counter, Christopher M. APPLICANT: Meyerson, Matthew APPLICANT: Weinberg, Robert A. TITLE OF INVENTION: Telomerase Cat NUMBER OF SEQUENCES: 52 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               Sequence 35, Application US/09026981 Sequence 35, Application US/09026981 GENERAL INFORMATION:
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pairs
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SEQUENCE 4023 BP; 668 A; 1363
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LENGTH: 4023
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OTHER INFORMATION: /note= "preliminary sequence for OTHER INFORMATION: human TRT cDNA insert of OTHER INFORMATION: plasmid pGRN121"
SEQUENCE 4029 BP; 687 A; 1342 C; 1255 G; 720 T; 25 OTHER.
                                                                                                             SOFTWARE: PACENTIN Release #1.0, Version #1.30 CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050 CLASSIFICATION: 536
PRILING DATE: 09-MAY-1997
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
                        STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    015389-002930US
                                                                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIPICATION: 536
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18 APR-1997
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-WAY-1997
CLASSIFICATION: 536
                                                                of America
                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01531
TELEPHONE: (415) 576-0200
TELEFRA: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                            Randolph T. 36,429
                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                               COUNTRY: United States ZIP: 94111
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Best Local Similarity 97.0%;
Matches 2754; Conservative
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MEDIUM TYPE: Floppy
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US-08-854-050-173 STANDARD; DNA; UNC; 4029
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APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Novel Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 173, Application US/08854050 Sequence 173, Application US/08854050 GENERAL INFORMATION:
APPLICANT: Cech, Thomas R. APPLICANT: Inigner, Joachim APPLICANT: Nakamura, Toru APPLICANT: Chapman, Karen B. APPLICANT: Morin C.
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2755 AGACAGIGGIGAACTICCCIGIAGAAGACGAGGCCCIGGGIGGCACGGCITITGIICAGA 2814
                                  TGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAA
                                                                                                                                                                   CCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGA
                           GCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCCACCACGCGTGCGCATCAGGG
                                                                                               GCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                   ALUKESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                          US-08-851-843-173 STANDARD; DNA; UNC; 4029
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Marin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
TITLE OF INVENTION: Novel Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
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APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 173, Application US/08851843
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PRIOR APPLICATION DATA:
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CLASSIFICATION:
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Pred. No. 0.00e+00;
0; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= "preliminary sequence for OTHER INFORMATION: human TRT cDNA insert of OTHER INFORMATION: plasmid pGRN121" SEQUENCE 4029 BP; 687 A; 1342 C; 1255 G; 720 T; 25 OTHER.
                                                                                                                                  015389-002930US
      08/724,643
APPLICATION NUMBER: US 08/724,
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: APPle, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01538
TELECOMMUNICATION INFORMATION:
TELEFRAN: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 97.0%;
Matches 2754; Conservative
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LOCATION: 1..4029
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AAACTICCCIGIAGAAGACGAGGCCCIGGGIGGCACGCCIITIGIICAGA 2814 AAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAG TTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGG SGTCAGGCAGCATCGGGAAGCCAGGCCGCCCTGCTGACGTCCAGACTCC ACGGAGGICATCGCCAGCATCATCAACCCCCAGAACACGTACTGCGTGC GTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCCTTCAAGAGCC SCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCA CTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCCA TACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGC ACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGA GTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCC AACTACGAGGGGGGGGGCCCCCGGCCTCCTGGGCGCCTCTGTGCTGG ATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGCGGGCCCCAGGACC CTGTACTTTGTCAAGGTGGATGTGACGGCGCGTACGACCATCCCCC TTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGG GTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCT

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                                                                                                      APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William
IITLE OF INVENTION: Telomerase Reverse Transcriptase
                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002500US
TELECOMMUNICATION INFORMATION:
                                RESULT 10
ID US-08-911-312-18 STANDARD; DNA; UNC; 3855
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
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APPLICATION NUMBER: US 08/854,050
FILING DATA: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                        Sequence 18, Application US/08911312
Sequence 18, Application US/08911312
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFEMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3855 base pairs
2831 TGCCGGCCCACGGCCTAT 2848
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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LOCATION: 56..
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                                                                                                                                                                                                                                                   121 GCCGCTGGCCACGTTCGTGCGGCGCCTTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG
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                                                                                              0; Indels 182;
                                                                 Length 3855;
OTHER INFORMATION: /product= "hrrr"
OTHER INFORMATION: /note= "clone #712562"
SEQUENCE 3855 BP; 651 A; 1300 C; 1226 G; 678 T; 0 OTHER.
                                                               DB 22;
                                                              Score 2444; DB 22;
Pred. No. 0.00e+00;
0; Mismatches 0
                                                            Query Match 85.8%;
Best Local Similarity 93.6%;
Matches 2655; Conservative
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QY 2052 CAGGGTGCTCAACTACGAGGGGGGGGGGGCCCCGGGCCTCCTGGGGCCCTGTGGGG 2111 Db 2101 CCTGGAGGATATCCACAGGGCCTGGCGCACCTTCGTGGCGTGTGCGGGCCCAGGACC 2160 L	Db 2161 GCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGTACGACACCATCCCCCA 2220 	Db 2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG	Db 2281 TCGGTATGCCGTGGTCCACAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340	2341 CGTC	DD 2344 2344 OY 2412 GACCAGCCGCTGAGGGATGCCGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAG 2471	2344	Db 2345CTACGTCCAGTGCCAGGGATCCCGCAGGCTCCATCCTCTCCACGTGCTCTG 2398	Db 2399 CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGGATTCGGCGGGACGGGCT 2458	Db 2459 GCTCCTGCGTTTGGTGGATGATTTCTTGTGGACACCTCACCTCACGCGAAAAC 2518 	Db 2519 CTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGGAA 2578	2579 GACAGIGGIGAACIICCCIGI 	Db 2639 GCGGCCCACGCCTAT 2655	RESULT 11 ID US-08-912-951-4 STANDARD; DNA; UNC; 3855 BP. AC XXXXXX	DE Sequence 4, Application US/08912951 CC Sequence 4, Application US/08912951 CC GENERAL INFORMATION:	CC APPLICANT: Cech, Thomas R. CC APPLICANT: Linguar, Joachim CC APPLICANT: Nakamura, Toru CC APPLICANT: Chapman, Karen B.	CC APPLICANT: MOTIN, Gregg B. CC APPLICANT: Harley, Calvin CC APPLICANT: Andrews, William H. CC TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND	CC TITLE OF INVENTION: THERAPEUTIC METHODS CC NUMBER OF SEQUENCES: 335 CC CORRESPONDENCE ADDRESS:
	1032 CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCTGCG 1091 1081 GCCCTCCTTCCTACCTACTCTGAGGCCCAGCTGACTGGCGCTCGGAGGCTGGA 1140 1092 GCCTCCTTCCTACTACAGCTCTCAGAGCTCAGCTTAACTACTAGAGAGCTCGAGATATAATAATAATAATAATAAATA	GACCATCTTCTGGGTTCCAGGCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCGCTTTCTGGGTTCCAGGCCTGGATGCCAGGACTCCCCGCAGGTTGCCCGCCTTTTCTGGGTTCCAGGATGCCAGGAACTCCCCGCAGGATGCCAGGAACTCCCGCAACTCCCGCAACTCCCGCAACTCCCGCAACTCCCCGCAACTACCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCGCAACTACCCCCACAACTACCCCCACAACTACCCCCACAACTACCCCCACAACTACCCCCACAACTACCCCCACAACTACCCCCACAACTACCCCCACAACTACCCCCC	GCCCAGCGCTACTGGCAAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA	1261 GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGC 1320	1321 AGCCGGTGTCTGTGCCCGGGAAGCCCCAGGCTCTGTGGCGGCCCCCGAGGAGGAGGAGA 1380 	1381 CACAGACCCCGTCGCTGCTGCTGCTGCTGCCAGCAGCAGCCCCTGGCAGGTGTA 1440	1441 CGGCTTCGTGCGGCCTGCGCCGGCTGGTGCCCCCCAGGCTCCTGGGGCTCCAGGC 1500	CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1	GCTCTCCCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCCTGGGGTAGCGAGAGCTGCCGCAGAGAGGGAGG	GAGCCCAGGGGTTGGCTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGAATCCTGGC 1		1741 TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG 1800 	1801 CAAGTIGCAAAGCATIGGAATCAGACAGCACTIGAAGAGGTGCAGCTGCGGGAGCTGTC 1860 	1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGCCCGCCC	1921 CTTCATCCCCAAGCCTGACGGGCTGCGGCTGATGTGAACATGGACTACGTGGGGGGC 1980 	1981 CAGAACGTTCCGCAGAGAAAAAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCATGTT 2040 	2041 CAGCGTGCTCAACTACGAGCGGGCGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGG 2100

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "nucleic acid sequence with an open reading frame encoding a delta-182 variant polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 85.8%; Score 2444; DB 22; Length 3855; Best Local Similarity 93.6%; Pred. No. 0.00e+00; Matches 2655; Conservative 0; Mismatches 0; Indels 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 56..2479
LOCATION: 56..2479
OTHER INFORMATION: /product- "delta-182 variant
OTHER INFORMATION: polypeptide"
SEQUENCE 3855 BP; 651 A; 1300 C; 1226 G; 678 T; 0 OTHER.
                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAITIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                              CURKERN APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 10-CCT-1996
CLASSIFICATION UNMBER: US 08/724,643
ATTORREY AGENT INFORMATION:
NAME: APPLICATION NUMBER: 35,429
REGISTATION NUMBER: 36,429
REGISTATION NUMBER: 36,429
REGISTATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 36,429
E: Townsend and Townsend and Crew Two Embarcadero Center, 8th Floor
                                 STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 576-0200
TELEPRAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3855 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                         San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
 ADDRESSEE:
STREET: TWC
CITY: San B
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                                                       181 GGACCCGGCGGCTTTCCGCGCGCGCTGGTGCCTGGTGCTTGCGTGCCCTGGGACGC
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QY 2292 TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA 2351	Db 2341 CGTC 2344 QY 2352 CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2411	Db 2344 2344 Oy 2412 GACCAGCCGCTGGTCGTCGTCGTCGAGAGAGCTCCTCCCTGAATGAGGCCAG 2471	Db 2344 2344 Qy 2472 CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG 2531	Db 2345CTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCCACGCTGCTG 2398 1111	Db 2399 CAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGGATTCGGCGGGACGGGCT 2458 	2459 GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCGCGAAAAC 2 	Db 2519 CTTCCTCAGGACCCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGACTTGCGGAA 2578 	Db 2579 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2638	Db 2639 GCCGCCCACGCCTAT 2655 	RESULT 12 ID US-08-912-951-6 STANDARD; DNA; UNC; 4200 BP. AC XXXXXXX	Sequence 6, Ap Sequence 6, Ap GENERAL INFOR		CANT: CANT: OF IN	TITLE OF INVENTION: THEKAPEUTIC ME NUMBER OF SEQUENCES: 335 CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend		CC COMPUTER READABLE FORM: CC MEDIUM TYPE: Floppy disk CC COMPUTER: IBM PC compatible		CC FILING DATE: 14-AUG-199/ CC CLASSIFICATION: 435
1201 GCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCA 1260	GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGTGCGGTCACCCCAGC	SGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCGCCCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGG	81 CACAGACCCCGTCGCCGGGGGGCGCCCCCGCGCGCCCCCGGCGCCCCCC	CGGCTTCGTGCGGCCTGCCTGCGCGGCTGGTGCCCCCCAGGCCTCTGGGGCTCCAGGC	CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAA 1 	1 GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGACTGCGCTTGGCTCGCGCAGCTGCGCAGCAGCAGGAGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGACTGCGCGGGACTGCGCTGCGCAGGAGATGAGCGTGCGGGACTGCGCTGCGCAGGAGAAGATGAGCGTGCGGGGACTGCGCTGCGCAGGAGATGAGCGTGCGGGACTGCGCTGCGCAGGAGATGAGCGTGCGGGACTGCGCTGCGCAGCAGATGAGCATGAGCAGGACAGCGGGACTGCGCTGCGCAGCAGCAGAAGATGAGCAGCAGGGACTGCGCTTGCGCTGCGCAG	1621 GAGCCCAGGGGTTGGCTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGC 1680	CTTTTA 	TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG	1801 CAAGTIGCAAAGCAIIGGAAICAGAACIIGAAGAGGGIGCAGCIGCGGGAGCIGIC 1860 	1861 GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGCCCGCCTGCTGACGTCCAGACTCCG 1920	1921 CTTCATCCCCAAGCCTGAGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGGAGC 1980 	1981 CAGAACGTTCCGCAGAGAAAAGAGGCCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT 2040 	2041 CAGCGTGCTCAACTACGAGCGGGGCGCGCCCCCGGCCTCTGGGCGCCTCTGTGCTGGG 2100	2101 CCTGGACGATATCCACAGGCCTGGCGCACCTTCGTGCTGCGGGTGCGGGCCCAGGACCC 2160 	2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA 2220	2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG	2281 TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA 2340

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3277 TGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCCGCCAGCACCACGCGGGGCCC 3336
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                                                                                                                  CGTGCTGGTTCACCTGCTGCCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGC
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SEQUENCE 4200 BP; 525 A; 1187 C; 1138 G; 644 T; 706 OTHER.
                                                                                                                                                                                                                                                                ATCORNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMINICATION INFORMATION:
TELEFORMINICATION OF 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4200 base pairs
TYPE: nucleic acid
STRANDENNES: single
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Pred. No. 0.00e+00;
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                                                        APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
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FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
US 08/854,050
           09-MAY-1997
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Best Local Similarity 94.0%;
Matches 1630; Conservative
                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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3877 CCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGA 3936
                             1527 CCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTGGCTGCAGGA
                                                          Sequence 1, Application US/09042460
Sequence 1, Application US/09042460
GENERAL INFORMATION:
APPLICANT: Morin, Gregg B.
APPLICANT: Allsopp, Richard
APPLICANT: Allsopp, Richard
APPLICANT: Greenberg, Roger
TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase
UNDER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                           STALL.

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,460

TILING DATE: 16-MAR-1998

TILING DATE: 16-MAR-1998
                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION AND APPLICATION DATA:
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US-09-042-460-1 STANDARD; DNA; UNC; 3496 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: WO PCT/US97/17885 FILING DATE: 01-OCT-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/974,549 FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
FRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
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Pred. No. 0.00e+00;
0; Mismatches 838; Indels 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 39.3404
OTHER INFORMATION: /Product- "mouse telomerase reverse OTHER INFORMATION: transcriptase (MTRI)"
SEQUENCE 3496 BP; 762 A; 998 C; 928 G; 808 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
NAME/KEY: 10..3435
COCATION: 10..3435
COTHER INFORMATION: /note= "mouse telomerase reverse
OTHER INFORMATION: transcriptase (mTRT) cDNA"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "mouse telomerase reverse OTHER INFORMATION: trascriptase (mTRT) cDNA clone" FEATURE:
                                                                           APPLICATION NUMBER: US 08/979,742
FILING DATE: 26-NOV-1997
ATORNEY/AGENT INFORMATION:
NAME: Elinborn, Gregory P.
REGISTRATION NUMBER: 38,440
REFENCE/DOCKET NUMBER: 015389-003110US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3496 base pairs
TYPE: nuclet acid
STRANDENESS: Single
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/979,742
                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 67.1%;
Matches 1901; Conservative
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LOCATION: 1..3496
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TTATCTTGTGCCCCCCAGCTGTGCCTACCAGGTGTGGGTCTCCCCT	CACCACGGATATCTGGCCCTCTGTGTCCGCTAGTTACAGGCCCAC	GACCCGIGGGCAGGAATTICACTAACCTIAGGITCTIACAACAGAICAAGAGCAGIA 	CCAGGAAGCACCGAAACCCCTGGCCTTGCCATCTCGAGGTACAAAGAGGCATCTGA 	CACCAGTACAAGTGTGCCTTCAGCTAAGAAGGCCAGATGCTATCCTGTCCGAGA 	ACCCACAGGGAGGTGCTACCAACCCATCAGGCAAATCATGGGTG 	CGGTCCCCCGAGGTGCCTACTGCAGAGAAAGATTTGTCTTCTAAAG 	CTGACCTGAGTCTCTGGGTCGGTGTGCTGTAAACACAAGC 	ACATCTCTGCTGTCACCACCCGCAAAATGCCTTTCAGCTCAGGCCATTAT 	CCAGACATTICCTTIACICCAGGGAGAIGGCCAAGAGCGTCIAAACCCCTCAIICCT	CTCAGCAACCTCCAGCCTAACTTGACTGGGGCCAGGAGACTGGTGGAGATCATCTTCT 	CAAGGCCTAGGACATCAGGACTCTGCAGGACACACCGTCTATCGCGTCG 	CAGATGCGGCCCTGTTCCAACAGCTGCTGGTGAACCATGCAGAGTGCCAATATGT 	CCTCAGGTCACATIGCAGGTTTCGAACAGCAAACCAACAGGTGACAGAIGCC 	GAACACCAGCCCAC	GGCTCTGTGGCGGCCCCCGAGGAGGAGGACACA	CATGGATTTGCTCCGCCTGCACAGCAGTCCCTGGCAGGTATATGGTTTCTTCG	CTGGGGTACCAGGCACAAI 	GGGGAAATACGGCAAGCT?	SAAGTICATCICCIGGGGAAGCAIGCCAAGCIC	SAAAGTAGAGGATTGCCACTGGCTCCGCAGCAGCCC
CIGIGCICTTIAICTICIG	GTACCAAATTTGTGCCACC	CCGACCCGTGGGCAGGAAT	TCGCCAGGAAGCACCGAAA CGTCAGGGGCGGGGTC	CT S	GGAGGAGCGCCACAGG	TCCTGCTCGGTCCCCCGAG	GTCTGACCTGAGTCTCTCT	CTCCACATCTCTGCTGTCA CCCCCCATCCACATCGCGG	GACCAGACATTTCCTTTAC	ACTCAGCAACCTCCAGCCT	GGGCTCAAGGCCTAGGACA 	CTGGCAGATGCGGCCCTG	CAGACTCCTCAGGTCACAT		TGCCCGGGAGAGCCCCAGGGCTCT	GCACCTCATGGATTTGCTC 111 1 11111 TCGCCTGGTGCAGCTGCTC	GGCCTGTCTCTGCAAGGTGGTGTCTGCTAGTCT 	일=		GGAACTGATGTGGAAGATGAAAG
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2414 1765 1823 1825 1885 1943 1945 2003 2005 2063 2065 2123 2125 2183 2185 2243 2245 2300 2305 2360 2365 2425 2474 2485 2534 2545 2594 2605 2654 2665 TTARGETTTGTTGATGACTTTCTGTTGGTGACGCTCACTTGGACCAAAAACCTT CCTGTGCTACGGCGACATGGAGAAGCTGTTTGCGGGGGATTCGGCGGGACGGGCTGCT GGAGGTTGTTGCCAATATGATCAGGCACTCGGAGAGCACGTACTGTATCGGCCAGTATGC 2244 GGAGGICATCGCCAGCAICATCAAACCCC---AGAACACGTACTGCGTGCGTCGGTATGC CAGCCTGTTTGACTTCTTCCTGCACTTCCTGCGTCACAGTGTCGTAAAGATTGGTGACAG GTGCTATACGCAGTGCCAGGGCATCCCCCAGGGCTCCAGCCTATCCACCCTGCTGCAG TCTGTGTTTCGGAGACATGGAGAACAAGCTGTTTGCTGAGGTGCAGCGGGATGGGTTGCT CTGGCTGATGGACACATACGTGGTACAGCTGCTTAGGTCATTCTTTTACATCACAGAGAG CATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGGAGCTGTCGGAAGCAGGGT GCCCAACGGCCTGCGGCCCATTGTGAACATGAGTTATAGCATGGGTACCAGAGCTTTGGG 1946 CAGAAGGAAGCAGCCCAGCATTTCACCCAGCGTCTCAAGACTCTTCAGCATGCTCAA GTACTTTGTTAAGGCAGATGTGACCGGGGCCTATGATGCCATCCCCCAGGGTAAGCTGGT 2246 AGTGGTCCGGAGAGATAGCCAAGGCCAAGTCCACAAGTCCTTTAGGAGACAGGTCACCAC CCTCTCTGACCTCCAGCCATACATGGGCCAGTTCCTTAAGCATCTGCAGGATTCAGATGC CATTGGAGTCAGGCAACACCTTGAGAGAGTGCGGCTACGGGAGCTGTCACAAGAGGAGGT CAGGCATCACCAGGACACCTGGCTAGCCATGCCCATCTGCAGACTGCGCTTCATCCCCAA 2426 2475 2486 2546 2606 2535 1764 1824 1886 2004 2184 2186 2361 2366 2595 1584 1586 1644 1646 1704 1706 1766 1826 1884 1944 2006 2064 2066 2124 2126 2306 g g a qq δλ g g g a a g δy g δy С οy q ò g ò g δ δ δ δ ŏ g QY g ò g à ò g ò ò δ

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Query Match
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                                                                        CCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTT
                                                          AGTGGTGAACTTCCCTGTGGAGCCTGGTACCTGGGTGGTGGAGCTCCATACCAGCTGCC
                     CCTCAGCACCCTGGTCCATGGCGTTCCTGAGTATGGGTGCATGATAAACTTGCAGAAGAC
                               2715 CCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGCCTGCGTGGTAAACTTGCGGAAAGAC
                                                                                                                                                                                                                               APPLICANT: Counter, Christopher M.
APPLICANT: Meyerson, Matthew
APPLICANT: Weinberg, Robert A.
TITLE OF INVENTION: Telomerase Catalytic Subunit Gene and
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                  Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T; 2 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,981
FILING DATE: 20-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Grandhan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH197-11p4AM
TELECOMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G; 735
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 20 FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/064,322
FILING DATE: 30-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,762
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 60/054,549
FILING DATE: 01-AUG-1997
FILING DATE: 01-AUG-1997
FILING DATE: 01-AUG-1997
FILING DATE: 01-AUG-1997
                                                                                                                                                          RESULT 14
ID US-09-026-981-36 STANDARD; DNA; UNC; 3346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/047,151
FILING DATE: 20-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/038,750
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear | SEQUENCE 3346 BP; 617 A; 1027 C; 965
                                                                                                                                                                                                   Sequence 36, Application US/09026981
                                                                                                                                                                                                          Sequence 36, Application US/09026981
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brood
STREET: Two Militia Drive
CITY: Lexington
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EDNESS: single
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                                                                                                       TGCTCACTGCCT 2797
                                                                                                                          2835 GGCCCACGCCT 2846
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                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                               STATE:
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                                                                                                         1640 GGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCC 1699
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                                                                                                                                                                                                                                                                                    TCAACTACGAGCGGGGGGGCGCCCCGGCCTCTGGGCGCCTCTGTGCTGGGCCCTCGGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1631 CCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTC----
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                                             0; Indels 182;
  Length 3346;
Score 816; DB 23;
Pred. No. 0.00e+00;
0; Mismatches 0
28.7%;
larity 84.9%;
Conservative
                      Similarity
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1689 GGCCAAGTICCTGCACTGGCTGATGAGTGTACTACCTCGTCGAGCTCCAGCTCTCAGGTTTCTT 1748
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                                                                                                                                                                                                                                                                                                                                                                                                                               121 GAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCT 180
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                                                                                                                                                                                                                                                                                                                                                                     61 TTATGICACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 CCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCCAGAACACGTACTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2229 CCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 GTTCAGCGTGCTCAACTACGAGCGGGGGGGGGCGCCCCGGCCTCCTGGGCGCCTCTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 CCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGAGAGTGTGACGGCGCGCGTACGACACCATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAAACATGGACTACGTCGTGGG
                                                                                                                                                                                                                                             Score 767; DB 22; Length 2176;
Pred. No. 0.00e+00;
0; Mismatches 0; Indels 182;
                                                                                                                                                                  NAME/KEY: -
LOCATION: 1..2176
OTHER INFORMATION: /note= "clone 712562"
SEQUENCE 2176 BP; 432 A; 678 C; 642 G; 422 T; 2 OTHER.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2176 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                            Query Match 26.9%;
Best Local Similarity 84.3%;
Matches 978; Conservative
                                                                                                                                     MOLECULE TYPE: CDNA
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APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
 TGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCC 1988
                                                                                                                      2780 TGAACTICCCTGTAGAAGACGAGGCCCTGGGTGGCAGCCTTTTGTTCAGATGCCGGCCC
                                             GGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGG
                                                                         2720 GGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PELICATION NUMBER: U$/08/912,951
FILING DATE: 14-AuG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: U$ 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor STREET: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
                                                                                                                                                                                                                                                           US-08-912-951-3 STANDARD; DNA; UNC; 2176 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DAYE.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/846,017
APPLICATION: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08912951 Sequence 3, Application US/08912951 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                   2840 ACGCCCTAT 2848
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2529 GGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGTGCT 2588
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                                                                                                                                                                                                                                        2769 GAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCA 2828
2469 CAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCCACCACGCCGTGCGCATCAG 2528
                                                                                                                                                                                                                           *** 899 GAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCA 958
                                                                                                                         779 GCTGCTCCTGCGTTTGGTGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAA
                       -----CTACGICCAGIGCCAGGGGAICCCGCAGGGCICCAICCICTCCACGCIGCI
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Search completed: Fri Dec 25 17:47:26 1998 Job time : 9031 secs.

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 $\rm n.\,a.$ $\rm \cdot n.\,a.$ database search, using Smith-Waterman algorithm with gap extension penalties as well as gap opening penalties MPsrch_nna

Fri Dec 25 15:11:23 1998; MasPar time 245.67 Seconds 540.766 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-951-733-13 (1-2848) from US08951733.seq (1 of 3) 2848 Title: Description: Perfect Score: N.A. Sequence:

1 CACGCGTCCGGGCACCCCTG.......GATGCCGGCCCACGGCCTAT 2848 GTGCGCAGGCCCGCTGCCGGGTA.

Scoring table:

TABLE default Gap open 30; Gap extend 1

Dbase 0; Query 0 Nmatch STD

88822 seqs, 23323279 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

n-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 9.326; Variance 5.654; scale 1.649

Statistics:

SUMMARIES

Adacta Length DB ID Description Pred. No. 2.4 7218 1 US-08-23- Sequence 14, Applicati 1.91e-14 1.2 215 1 US-08-23- Sequence 14, Applicati 1.91e-14 1.2 215 1 US-08-23- Sequence 5, Applicati 1.91e-14 1.2 215 1 US-08-23- Sequence 5, Applicati 1.91e-14 1.2 215 1 US-08-23- Sequence 5, Applicati 1.91e-16 1.2 215 1 US-08-23- Sequence 5, Applicati 2.32e-01 0.9 68 1 US-08-471- Sequence 243, Applicati 2.32e-01 0.9 74 2 PCT-US95-1 Sequence 100, Applicat 2.32e-01 0.9 74 2 PCT-US95-1 Sequence 94, Applicati 7.68e-02 0.9 74 2 PCT-US95-1 Sequence 99, Applicati 7.68e-02 0.9 75 2 PCT-US95-1 Sequence 99, Applicati 7.68e-02 0.9 81 2 PCT-US95-1 Sequence 99, Applicati 7.68e-02 0.9 81 2 PCT-US95-1 Sequence 98, Applicati 7.68e-02 0.9 81 2 PCT-US95-1 Sequence 98, Applicati 7.68e-02 0.9 81 2 PCT-US95-1 Sequence 98, Applicati 7.68e-02 0.9 82 2 PCT-US95-1 Sequence 99, Applicati 7.68e-02 0.9 82 2 PCT-US95-1 Sequence 97, Applicati 7.68e-02 0.9 82 2 PCT-US95-1 Sequence 0
7218 1 US-08-232 Sequence 14, Applicati 2 US-08-232 Sequence 5, Applicati 2 US-08-238 Sequence 5, Applicati 1 US-08-238 Sequence 5, Applicati 2 US-08-238 Sequence 5, Applicati 0 US-08-471 Sequence 142, Applicat 2 US-07-977 Sequence 142, Applicat 2 US-08-471 Sequence 142, Applicat 2 PCT-US95-1 Sequence 100, Applicat 2 PCT-US95-1 Sequence 100, Applicat 2 PCT-US95-1 Sequence 94, Applicati 2 PCT-US95-1 Sequence 94, Applicati 2 PCT-US95-1 Sequence 94, Applicati 2 PCT-US95-1 Sequence 99, Applicati 2 PCT-US95-1 Sequence 97, Applicati 7 Sequence
7218 1 US-08-232- Sequence 14, Applicati 1 US-08-238- Sequence 5, Applicatio 5 US-08-238- Sequence 5, Applicatio 6 US-08-428- Sequence 5, Applicatio 1 US-08-471- Sequence 14, Applicatio 1 US-08-471- Sequence 142, Applicatio 2 US-07-977- Sequence 142, Applicatio 2 US-07-97- Sequence 142, Application 2 US-07-95-1 Sequence 100, Application 2 PCT-US95-1 Sequence 94, Application 2 PCT-US95-1 Sequence 99, Application 3 US95-1 Sequence 97, Application 3 US95-1 U
215 1 US-08-238- Sequence 5, Applicatio 6 1 US-08-238- Sequence 5, Applicatio 1 US-08-471- Sequence 144, Applicatio 1 US-08-471- Sequence 144, Applicatio 2 0 1 US-08-471- Sequence 142, Applicat 2 PCT-US95-1 Sequence 94, Applicat 2 PCT-US95-1 Sequence 100, Applicat 1 74 2 PCT-US95-1 Sequence 94, Applicat 1 7 2 PCT-US95-1 Sequence 94, Applicat 1 7 2 PCT-US95-1 Sequence 94, Applicat 1 7 2 PCT-US95-1 Sequence 99, Applicat 1 2 PCT-US95-1 Sequence 99, Applicat 1 2 PCT-US95-1 Sequence 99, Applicat 1 2 PCT-US95-1 Sequence 98, Applicat 1 2 PCT-US95-1 Sequence 99, Applicat 1 2 PCT-US95-1 Sequence 99, Applicat 1 2 PCT-US95-1 Sequence 97, Applicat 1 7 Sequence 97,
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Sequence 97, Applicati 7
Sequence 97, Applicati 7

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٠,	Sequence 1, Applicatio	Sequence 7, Applicatio	~	'n	95,	145,	93, A	144,	143,	142,	25, A	25,	120,	25	18,	ų	٠.	Patent No. 5171840.	Sequence 11, Applicati	Sequence 11, Applicati		Patent No. 5480796.	Patent No. 5457037.	Sequence 1, Applicatio		Patent No. 5457037.
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ALIGNMENTS

Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
CE PATCHANT: BORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: SCHEIFLINGER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDERS: FOLGY & Lardner STREET: 1800 Diagonal Road, Suite 500
CITT: Alexandria STARE: Alexandria STARE: USA
COUNTRY: USA
ZIR: 23313-099
COUNTRY: USA
ZIR: PREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BAEABABLE FORM:
MEDIUM TYPE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION UNBER: US/08/232,463
FILING DATE:
CLASSIFICATION UNBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REFERRENCE/OCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION: US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP. TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEFAX: (703)683-4109 TELEX: 899149 INFORMATION FOR SEQ ID NO: 14: RESULT

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GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: LABANITCH,
APPLICANT: LABANITCH,
APPLICANT: LOGELL, Ann
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                               2019 GGCCCTCTTTTCTCTGCGGAACGTTCTGGCTCCCACGACGTAGTCCATGATCGG 1960
                                                                                                                                                                                                                                                                                                                                                                                                                                    1899 TICCCGATGCTGCCTGACACTTCCGACAGCTCCCGCAGCTGCACCTCTTCAAGTG 1840
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                                                                                                                                                                                                                            CLONE: pTZgpt-F1s
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
                                                                                                                                                                                                                                                                Length 7218;
                                                                                                                                                                                                                                                                                       165; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                        FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUINCATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 3
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP
              EP 91 114 300.6
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                                                                                                                                        14:
                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                         single
  FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                  linear
                                                                                                                                                                                                              IMMEDIATE SOURCE
                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                                                              1221 CTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTA 1280
                                                                                                                                                                              Gaps
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                                                                      CLONE: PIZGPL-FIS
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
                                                                                                             Juery Match 2.4%; Score 67; DB 1; Length 7218;
Best Local Similarity 2.4%; Pred. No. 2.08e-25;
Matches 9; Conservative 211; Mismatches 153; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TILLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SECULORES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                   linear
                                                  TOPOLOGY: lines
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: /Standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 144, Application US/08471052A
Sequence 144, Application US/08471052A
Patent No. S625033
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: FOWLKES, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
UNMERS OF SNOURNES: 166
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.2%; Score 35; DB 1; Length 215; Best Local Similarity 13.2%; Pred. No. 1.76e-06; Matches 26; Conservative 76; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JT 5
US-08-471-052A-144 STANDARD; DNA; UNC; 66 BP.
                NAME: Bastlan, Kevin L.
REGISTRATION NUMBER: 34,774
REFRENCE/CDCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEFAN: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/471,052A FILING DATE: 06-JUNE-1995 CLASSIFICATION: 530 ATTONENY/AGENT INFORMATION: NAME: MISTOCK, S. LESILE REGISTRATION NUMBER: 18,872
     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::::: | || :::::
1435 TGCTGTGCTGGCGGAGC 1419
                                                                                                                                                                                                   SS: single
unknown
                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 KSNVSNNCGGGNKRDVS 202
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APPLICANT: BENNETT, Alan
APPLICANT: LABAUTICH, John M.
APPLICANT: LABAUTICH, JOHN M.
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CORRESPONDENCE ADDRESS: 24
CORRESPONDENCE ADDRESS: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, one Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 SRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGTKSNVSNNCGGGNKRDVS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 HTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTAMTSRNRTGKTANNAVD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.2%; Score 34; DB 1; Length 215; Best Local Similarity 12.9%; Pred. No. 6.10e-06; Matches 17; Conservative 56; Mismatches 59; Indels
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COUNTRY: US
2 IP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T. 4
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
                                                                                                                           2307E-540
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFTCATION: 800
                                            CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BASTIEN, Kevin L.
REGISTRATION NUMBER: 34,774
REFECCOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-560
TELEFAX: (415) 543-5643
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
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STATE: California
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250 GCACGGCCGCC 261
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Sequence 142, Application US/08471052A
Sequence 142, Application US/08471052A
Sequence 142, Application US/08471052A
Sequence 142, Application US/08471052A
PAPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue
                                                                                                                                        Query Match 0.9%; Score 25; DB 1; Length 69; Best Local Similarity 11.3%; Pred. No. 2.32e-01; Matches 7; Conservative 18; Mismatches 37; Indels
                                                                                       Score 25; DB 1; Length 68;
Pred. No. 2.32e-01;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 CITIT: New YORK
COUNTRY: U.S.A.
2IP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: O6-JUNE-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK S. Leslie
REGISCHARTION NUMBER: 1101-179
TELEPRATION NUMBER: 1101-179
TELEPRATION NUMBER: 1101-179
TELEPRATION NUMBER: 120-9090
TELEPRAX: 212 869-8864/9741
TELEPRAX: 212 869-8864/9741
TELEPRAX: 05 D NO: 142:
SEQUENCE CHRARACTERISTICS:
LENTH: 69 DSSES
                                      TOPOLOGY: LINEAR
ANTI-SENSE: NO
SEQUENCE 68 BP; 7 A; 38 C; 17 G; 6 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA
SEQUENCE 69 BP; 2 A; 4 C; 6 G; 2 T; 55 OTHER.
                                                                                       Query Match 0.9%;
Best Local Similarity 75.5%;
Matches 37; Conservative
           TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                            STRANDEDNESS:
     LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1492 GG 1493
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APPLICANT: Ala-Kokko, Leena
APPLICANT: Ala-Kokko, Leena
APPLICANT: Williams, Charlene J.
APPLICANT: Baldwin, Clinton
APPLICANT: Baldwin, Clinton
APPLICANT: Ahmad, Nilofer Nina
TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
TITLE OF INVENTION: MEDISPOSITION FOR OSTEOARTHRITIS
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                            Score 25; DB 1; Length 66; Pred. No. 2.32e-01; 18; Mismatches 37; Indels
                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: DNA
SEQUENCE 66 BP; 2 A; 3 C; 4 G; 2 T; 55 OTHER.
                                                                                                                                                                                                                                                                                                                                          ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordferfect 5.1
CURRENT APPLICATION NAMER: US/07/977,284A
FILING DATE: 13-NOV-1992
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NAMER:
REFERENCE/DOCKET NUMBER: 1101-179
TELECHONIC: 212 790-9090
TELEFAX: 212 869-8864/9741
TELERA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 bases
TYPE: nucleic acid
STRANDEDNESS: single
STORDIGEY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TJU-0697
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 243, Application US/07977284A
Sequence 243, Application US/07977284A
Patent No. 5558988
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: DeLuca, Mark
REGISTATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-(TELECOMMUNICATION INFORMATION: TELEPAX: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 243:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                           Query Match 0.9%;
Best Local Similarity 11.3%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                        Sequence 94, Application PC/TUS9511934
Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICAMY: Cytogen Corporation
TITLE OF INVENTION: Partigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
SITRET: 1155 Avenue of the Americas
CITY: New York
SIATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 100, Application PC/TUS9511934
Sequence 100, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26; DB 2; Length 74;
Pred. No. 7.68e-02;
19; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CHELICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7T 9
PCT-US95-11934-100 STANDARD; DNA; UNC; 74 BP.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 11.48;
                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036
COMPUTER READABLE FORM:
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                                                 XXXXX
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RESULT
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945 CCACTCCCACCCATCGTGGGCCGCCAGCACCACGGGGCCCCCCATCCACATCGCGGCC 1004
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Sequence 100, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: CYPTOSON COMPORATION
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 2; Length 74;
Pred. No. 2.32e-01;
20; Mismatches 40; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ELOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036
COMPUTER READABLE FORM:
MEDIOW TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JT 10
PCT-US95-11934-100 STANDARD; DNA; UNC; 74 BP.
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ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
                                                                                                                                                                                                                                                                                                                           1101-196-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-1
TELECOMUNICATION INFORMATION:
TELERAX: (212) 790-9090
TELERAX: (614) PENNIE
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 0.9%;
Best Local Similarity 7.7%;
Matches 5; Conservative
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167 AGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGT 226
                                                 540 GAGCGCGCAGCAGCAGCAGGTGAACCAGCACGTCGTCGCCCACGCGGCGCAGCAGCAG 481
                 Sequence 99, Application PC/TUS9511934
Sequence 99, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 2; Length 75;
Pred. No. 2.32e-01;
20; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934 FILING DATE: 20-SEP-1995 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER.
                                                                                                                                                                     T 12
PCT-US95-11934-99 STANDARD; DNA; UNC; 75 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 13
PCT-US95-11934-99 STANDARD; DNA; UNC; 75 BP.
                                                                                                                                                                                                                                                                                                                                                                 E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 99, Application PC/TUS9511934
Sequence 99, Application PC/TUS9511934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 10.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 GCCTGGTGTG 236
                                                                                                                  480 CCCCCACGCC 471
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                                                                                 63 BNNBNACGCC 72
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                                                                                                                                                                                                      XXXXXX
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                                                                                                                                                                                                                                                                               Sequence 94, Application PC/TUS9511934
C Sequence 94, Application PC/TUS9511934
C SEQUENCE INFORMATION:
C TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
C TITLE OF SEQUENCES: 103
C CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
C STREET: 1155 Avenue of the Americas
C CTY: New York
C COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 7.68e-02;
19; Mismatches 43; Indels
                                                                                                                                                                                                                Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

COFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NATA:

APPLICATION NUMBER: PCT/US95/11934

FILING DATE: 20-SEP-1995
                                                                                                                                                                                                            Score 26; DB 2; L
Pred. No. 7.68e-02;
20; Mismatches 41
                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP: 6 A; 6 C; 1 G; 1 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                .T 11
PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1101-196-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 790-9090
TELERAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
             TELEPHONE: (212) 790-9090
TELERAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                 LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                              / Match 0.9%;
Local Similarity 10.3%;
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.9%;
Best Local Similarity 11.4%;
Matches 8; Conservative
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                 ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 11(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 81 base pairs
                                                                                                                                                                                                                                                 linear
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2508 CCACCACGCC 2517
                                           FILING DATE: 2 CLASSIFICATION:
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     0; Gaps
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 92, Application PC/TUS9511934
Sequence 92, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICAMT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCE: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.9%; Score 25; DB 2; Length 75; Best Local Similarity 10.0%; Pred. No. 2.32e-01; Matches 7; Conservative 20; Mismatches 43; Indels
                                                                                                                 COUNTRY: New YOLK
COUNTRY: New YOLK
COUNTRY: USA
ZID: 10006
COMPUTER: USA
COMPUTER: ELDAPH disk
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COMPUTER: PATHOLY DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATSORNEY/AGENT INFORMATION:
NAME: MASTOCK: S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET UNMBER: 1101-196-228
TELEPHONE: (212) 790-9090
TELEPAX: (212) 700-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
SEQUENCE 75 BP; 1 A; 1 C; 7 G; 5 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 14
PCT-US95-11934-92 STANDARD; DNA; UNC; 81 BP
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
CUUNTRY: USA
ZIP: 10036
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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C Sequence 98, Application PC/TUS9511934

C GENERAL INFORMATION:

APPLICANT: Cytogen Corporation

TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From

TITLE OF INVENTION: Peptide Libraries

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

C CITY: New York

C COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                      Query Match

0.9%; Score 26; DB 2; Length 81;
Best Local Similarity 11.4%; Pred. No. 7.68e-02;
Matches 8; Conservative 19; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.
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PCT-US95-11934-98 STANDARD; DNA; UNC; 81 BP.
XXXXXX
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                                                                                                          1101-196-228
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
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CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
SQ SEQUENCE 81 BP; 6 A; 6 C; 4 G; 5 T; 60 OTHER.

Query Match
Query Match
Best Local Similarity 7.7%; Pred. No. 2.32e-01;
Matches 5; Conservative 20; Mismatches 40; Indels 0; Gaps
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Search completed: Fri Dec 25 15:16:36 1998 Job time : 313 secs.

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	**************************************	8 1998; MasPar t 726.145	Title: >US-08-951-733-13 Description: (1-1920) from US08951733.seq (1 of 2) Perfect Score: 1920 N.A. Sequence: 1 CACGCGTCGGGCAGCGCTG	Gap open 30; Gap extend 1 Nmatch STD : Dbase 0; Query 0	Searched: 567134 seqs, 1101898692 bases x 2	ocessing:	Database: embl55 l:em_ba 2:em_fun 3:em_htg 4:em_huml 5:em_hum2 6:em_in 7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl 13:em_ro 14:em_vi Database: genbank107 15:gb_ba1 16:gb_ba2 17:gb_htg 18:gb_in 19:gb_om 20:gb_ov 21:gb_pat 22:gb_ph 23:gb_pl1 24:gb_pl2 25:gb_pr1 26:gb_pr2 27:gb_pr3 28:gb_ro 29:gb_st 31:gb_sy 32:gb_htg 33:gb_ro 33:gb_ro 33:gb_ro 33:gb_st 31:gb_sy	Statistics: Mean 11.310; Variance 6.127; scale 1.846	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES Basult	Score Match Length DB ID Description Proceedings of the Match Length DB ID Description Proceedings (1999) 99.4 4015 27 AF01595 Homo sapiens telomeras (1895 98.7 4027 27 AF018167 Homo sapiens telomeras (453 23.6 3426 28 AF051911 Mus musculus telomeras (110 5 7 2011 28 AF073311 Mus musculus telomeras (110 5 7 2011 28 AF0703311 Musculus telomeras (110 5 7 2011 28 AF0703311 Musculus telomeras (110 5 7 2011 28 AF0703311 Musculus telomeras (110 5 7 20 5 7 20 20 5 7 20 20 5 7 20 20 5 7 20 20 5 7 20 20 5 7 20 20 5 7 20 20 20 5 7 20 20 5 7 20 20 20 5 7 20 20 20 20 20 20 20 20 20 20 20 20 20	5 7218 21 166494 Sequence 14 1

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73333777777777777777777777777777777777	ALI 4015 bp telomerase intochondri	Moris hnoris 11741, 128), 00, 00, 00, 00, 00, 00, 00, 00, 00, 0	"hTR _sta
A10158 A10161 A10162 A10162 A10159 E04076 HVACO04787 MVU92534 HSARSIR22T SPUNK4 SPOTSE11 HS179D3A E04076 HS4BHLF CHKDILRB SMPROBAG AF034863 AF0314863 AF011922 MTY20H10 AF011922 MTY20H10 AF011922 MTY20H10 AF011922 MTY20H10 AF0134863 AF011922 MTY20H10 AF0134863 AF011922 MTY20H10 AF01365 HSN5H6 AF01365 HSN5H6 AF0033117 HSN5H6 AF0033117 HSN5H6 AF0033117 HSN5H6 AF0933117 HSN5H6 AF093117 AF1362 AF1363 AF	9 4 62	1 to 4015) C.M., Morin, G.B., Chapman, K.E. H., Lingmer, J., Harley, C.B. catalytic subunit homologs 77 (5328), 955-959 (1997) 1 to 4015) mission (24-94015, USA coatlon/Qualifiers L., CA 94015 Corganism="Homo sapiens" (4015 Corganism="Homo sapiens" (4015 Corganism="Homo sapiens" (4015 Cheromosome="5" Chromosome="5" L., 4015 L., 4015	TRT" tart=1
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BASE COUNT ORIGIN

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Qy	672	TGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGCCTGCCAGCCCCGGGTGCGAG
Dp	721	GTIGCCCAAGAGGCCCAGGCGIGGCGC 78
δλ	732	AGGCGCGGGGCCAGTGCCAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGC 7
g :	781	SGCCCACCGGGCAGGAC 8-
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qq	4	SAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAAGAAGC
ΟŊ		CGTGGACCGAGTGACCGTGGTTTCTGTGTGTGTCACCTGCCAGACCCGCGGAAGAAGC 91
qq	901	CITTGGAGGGGCCCTCTCTGGCACGCCCACTCCCACCCATCCGTGGGCCGCCA 96
QY	912	Accicinida Agadencici caca cacacaca con con a con a con contra con a contra con contra
qq	196	CCACGCGGGCCCCCCATCCACATCGCGGCCACCACCTCCCTGGGACACGCCTTGTCC 1
QY	972	CACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTC
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δÿ	1032	CCGGTGTACGCCGAGACCAAGACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGC
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λŏ		CATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCGCCT 121
q		CCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAAGCACGCGCA 126
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δ	1692	CAAGTICCIGCACIGGCTGAIGAGIGIGIACGICGICGAGCIGCICAGGICTITCITITÀ 175
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                                                                                                                                                                                                                                                            Synthetic construct human telomerase catalytic subunit (hTERI/hESI2) mRNA and 3' Influenza A hemagglutinin tag, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haber, D.A. and Weinberg, R.A. Telomerase activity is restored in human cells by ectopic expression of hTERT (hEST2), the catalytic subunit of telomerase oncogene 16 (9), 1217-1222 (1998)
                                                                                                                                                                                                                                                                                                                                                                       synthetic construct.
synthetic construct
artificial sequence.
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Counter, C.M., Meyerson, M., Eaton, E.N., Ellisen, L.W., Caddle, S.D.
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Haber, D. and Meinberg, R.A.
Elliset, Submission
Submitted (20-0AN-1998) Whitehead Institute, 9 Cambridge Center, Cambridge, MA 02142, USA
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NEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTILCSLCYGDMENKLFAG
IRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFFYEDEAL
GGTAFVQMPAHGLFPWGGLLDTRTLEVQSDYSSYARSITRASLTFNRGFKAGRNMRR
KLFGVLRLKCHSLFLDLQVNSLQTVCTTIXILLLQAYRFHACVLQLPFHQOWNRPT
FELRYTSDTASLCYSILKAKRAGAMSLGAAGPLPSEAVQMTCHQAFLLKLTRHRVT
YVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILDYPYDVPDYAGYPD
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                                                                                                                         Veuron. 4605
/hote="engineered based on the epitope for the anti-influenza virus hemagglutinin monoclonal antibody 12CA5; similar to part of the Influenza A hemaglutinin mane sequence in GenBank Accession Number M29257"
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Pred. No. 0.00e+00;
0; Mismatches 2;
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/db_xref="taxon:32630"
2551 c 2484 g 2038 t
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Meyerson,M., Counter,C.M., Eaton,E.N., Ellisen,L.W., Steiner,P.,
Caddle,S.D., Ziaugra,L., Beijersbergen,R.L., Davidoff,M.J., Liu,Q.,
Bacchetti,S., Haber,D.A. and Weinberg,R.A.
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KLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPT
FFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLLKKLTRHRVT
                                                                                                                                                                                                                                                                                                                       Meyerson, M., Counter, C.M., Eaton, E.N., Ellisen, L.W., Steiner, P., Caddle, S.D., Ziaugra, L., Beijersbergen, R.L., Davidoff, M.J., Liu, Q., Bacchetti, S., Haber, D.A. and Weinberg, R.A.
hEST2, the putative human telomerase catalytic submit gene, is up-regulated in tumor cells and during immortalization
Cell 90 (4), 785-795 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="telomerase catalytic subunit"
/db_xref="PID:92347129"
/translation="MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDP
                                                                                              29-AUG-1997
mRNA, complete
                                                                                                                                                                                                                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/note="member of reverse transcriptase
/codon_start=1
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/note="human Ever Shorter Telomeres
/gene="hbsF12"
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GGTCAGGCAGCATCGGGAAGCCAGGCCGCCCTGCTGACG 1920
                                                                                                               telomerase catalytic subunit
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/chromosome="5"
/map="5p15.33"
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                                     801 GCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACC
                                                                        GAGTGACCGTGGTTTCTGTGTGTGTCACCTGCCAGACCCGCCGAAGAAGCCACCTCTTT
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109	115	121	127	133	139	145	151	157 158	163	169	175	181	187	JULT JUNI SERE SERE	OURNA
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Greenberg, R.A., Allsopp, R.C., Chin, L., Morin, G.B. and DePinho, R.A.
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Submitted (19-JUN-1998) Immunology and Oncology, National Centre
Biotechnology, Cantoblanco, Madrid 28049, Spain
Location/Qualifiers
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                                                                                           CACGTITCAAAAGAACAGGCTCTITITCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAG 1823
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Bukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 3369)
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Martin-Rivera,L., Herrera,E. and Blasco,M.A.
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house mouse. Mus musculus

NID KEYWORDS SOURCE ORGANISM

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/product="telomerase catalytic subunit"
/db_xref="PlD:92605903"
/translation="FFYOFESFORNELFFYRKSVWSKLQSIGVRQHLERVRELSG
EFVRHADTWLAMPCELRFIPK"

1 t
                                                                                                                                  Drissi, R. and Cleveland, J.L.
Drisct Submission
Submitted (07-007-1997) Biochemistry, St jude Children's Research
Hospital, 332 North Lauderdale, Memphis, TN 38105, USA
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 201)
Drissi, R. and Cleveland, J.L.
Partial sequence of Mus musculus telomerase catalytic subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 201;
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Pred. No. 3.62e-55;
0; Mismatches 31; Indels
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Dorner,F., Schelflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
/cell_line="32D.3"
                                                                                                                                                                                                                                       Location/Qualifiers
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1491 c 1486 g
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                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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Best Local Similarity 82.0%;
Matches 141; Conservative
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Unclassified.
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Unpublished
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Best Local Similarity
Matches 9; Conser
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Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System Unpublished
3 (bases 1 to 74371)
Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Davis, C.A., Kadner, K., Miguel, T., Pitluck, S., Pollard, M., Rojeski, H., Subramanian, S. and Martin, C.H.
                                                                                                      Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primetes; Catarrhin; Hominidae; Homo.

1 (bases 1 to 74371)

Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Radher,K., Miquel,T., Miller,C., Pitluck,S., Pollard,M., Subramanian,S. and Martin,C.H..

Sequencing of human chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-MUG-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A.
DOE Joint Genome Institute...
Location/Qualifiers
L. 74371
/organism."Homo sapiens"
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/note="65% & 69% protein identity GenPept:U22377"
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8258. .8503
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97070. .9387
/rpt_family="Alu"
complement(9740. .9845)
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join(3246. .3410,3721. .3828)
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2295. .2438
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2818. .2859
/note="(GT)21"
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/rpt_family="Alu"
5586. .6956
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complement(7830.
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893. .1030
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/rpt_family="Alu"
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rpt_family="L1"
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note="(CA)19"
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/note="(A)22"
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                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                       Homo sapiens
                                                                                                                                                                                                                                    Unpublished
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sequence.
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                                                                                     ORGANISM
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JOURNAL
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AUTHORS
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AUTHORS
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JOURNAL
               ACCESSION
                              NID
KEYWORDS
SOURCE
                                                                                                                                          REFERENCE
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                                                                                                                                                                                  1161 TCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCG 1220
                                                                                                                                                                                                                                                          1221 CTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCTA 1280
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                                                                                   CCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGAGACCATCTT 1160
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             23-DEC-1997
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                    PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="unknown"
1491 c 1486 g 1929 t
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Sequence 14 from patent US 5670367.
166494
92724471
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ACCESSION
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ORGANISM
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TITLE
JOURNAL
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ORIGIN
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RESULT

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2022. 23326
23473. 23761
23473. 23761
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complement(10440. .11015)
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complement (25349. .25713)

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27774. .28056

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21736. .22035
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:omplement(22638. .22981)
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complement(16993. .17085)
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/note="(AC)12"

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19914. 19945
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complement(24639.
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complement(3755. 37554)

Complement(3755. 37554)

Anote="GRAIL 2 excellent exon, frame 0" 38578,38741. 38995, 39071. 3205,35952. 38678. 38462. 38578,38741. 38995, 39071. 3205,35952. 39630,39935. 40048,40300. 40410,40503. 40661,41868. 41972,42103. 42225,42492. 42569,44379. 44507))

Astandard.name="histidyl-tRNA synthetase" // frandard.name="histidyl-tRNA synthetase" // note="78%-100% protein identity GenPept:U18937" // note="GRAIL 2 excellent exon, frame 0" complement(38462. 38215)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 15955 CKSSKCWCWSYRMRNKCYSCSYCYCSSGKKYWCRCSMYWYTCYYSYKYYWSMSYCTCTSW 16014
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Pred. No. 5.98e-06;
50; Mismatches 25; Indels 0
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complement(34021. .34144)

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(Ab_xref="dbsST:AI025011"
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DEFINITION Sequence 5 from patent US 5569830.
ACCESSION 128278
SIB19054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 16015 GWRWMWSKGRSWMYASRSGCSCSCSMC 16041
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GCCACTCAGGCCCGGCCCCGCCACAC 633
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/rpt_type=tandem
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Best Local Similarity 13.8%;
Matches 12; Conservative
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AC005369 74371 bp DNA .... PRI 01-AUG-1998
Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete
                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Erimates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 74371)
Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Kadner, K., Miguel, T., Miller, C., Pitluck, S., Pollard, M., Sojeski, H., Subramanian, S. and Martin, C.H.
Sequencing of human chromosome 5

    (Losses 1 to 1701)
    Ricke, D.O.
    Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System

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Joseph London, Control of Street

Rimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M.,

Bavis, C.C.A., Kadner, K., Miguel, T., Pitluck, S., Pollard, M.,

Rojeski, H., Subramanian, S. and Martin, C.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-M0G-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A.
Sequence submitted by:
DOE Joint Genome Institute.
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2295. 2438
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2295. 2438
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2818. 2859
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                                                                                                                                                                                                                                                                         Unpublished
2 (bases 1 to 74371)
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AUTHORS
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1 (Dases 1 to 215)

1 (Dases 1 to 215)

Bennett, J. Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 9-02T-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 215)
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
                                                                                                                                                                                                                                                                                                                        83 HTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTAMTSRNRTGKTANNAVD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 YNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKT 125
                                                                                                                                                                                                                                                                                                                                             126 AMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGT 185
                                                                                                                                                                                                                                                                                                                                                                                           143 SRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGTKSNVSNNCGGGNKRDVS 202
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Pred. No. 8.13e-05;
76; Mismatches 95; Indels
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Pred. No. 2.93e-04;
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Sequence 5 from patent US 5569830.
128278
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Best Local Similarity 13.2%;
Matches 26; Conservative
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Best Local Similarity 12.9%;
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complement(10440. 11015)
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complement(16993, .17085)
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complement(17678, .18276)
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19305, .19583
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complement(25349. .25713)
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complement(25727. .26471)
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complement(19943. .20222)
/rpt_family="Alu"
21202. .21496
                                                                                                                                                                        /rpt_family="Alu"
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/note="(A)29"

/note=tendem

/rpt_unit=A

12365. .12645

/rpt_family="Alu"

13727. .13727

/note="(AC)12"
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13783. 14024
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14175. 14470
/rpt_family="Alu"
complement(14906.
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21736. .22035
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22017. .22038
/note="(A)22"
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/rpt_unit=A
complement(24639.
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/rpt_family="Alu"
complement(22638.
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9914. .19945
                                'rpt_family="Alu"
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/note="(GTTT)8"
/rpt_type=tandem
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/rpt_unit=A
/2321. .22457
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36901. 37164
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/note="GRAIL 2 excellent exon, frame 0"
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39071. 32205,39532. 39630,39935. 40048,40300. 40410,
40503. 446661,41868. 41972,42103. 42225,42492. 42569,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 15923 STSKCSCMSRSKSKRGWGYRSWKKYRCAMWMTCKSSKCWCWSYRMRKCYSCSYCYCSSG 15982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15983 KKYWCRCSMYWITCYYSYKYYWSMSYCTCTSWGWRWMWSKGRSWMYASRSGCSCSCSMCM 16042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1620 AGCGCAGTCCCGCACGCTCATCTTCCACGTCAGCTCCTGCAGCGAGAGCTTGGCATGCTT 1561
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//note="78%-100% protein identity GenPept:U18937"
complement(38069. 38215)
/note="GRAIL 2 excellent exon, frame 0"
                                                                                                                                                                                                                          /rpt_family="Alu"
join(29465. .29559,29598. .29779)
//oote="95% identity dbsTs:G14522 (SHGC-11312)"
29495. .29976
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Pred. No. 2.93e-04;
92; Mismatches 89; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="Alu"
32977. 33088
/rpt_family="MLT1"
complement(38670. 33785)
/rpt_family="Alu"
complement(3401. 34144)
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/note="GRAIL 2 excellent exon, frame 1"
/note="GRAIL 2 excellent exon, frame 1"
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complement(30682. 30733)
//pt_family="MIR"
complement(31573. 31724)
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complement(32159. .32232)
Moote-"GRAIL 2 excellent exon, frame 2"
32388. .32488
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                                                                                                      28712. .28930
/rpt_family="MER20"
complement(28769. .28838)
/note="GRAIL 2 excellent exon, frame (
28987. .29214
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/note="100% identity EST ov84a10.x1"
complement(30401. .30536)
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rpt_family="Alu"

86901. .3722

/note="100% identity EST ou55c09.x1"

86901. .37164
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2617. .32908
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/rpt_family="Alu"
28040. .28066
/note="(A)27"
                                                                     'rpt_type=tandem
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Best Local Similarity 14.6%;
Matches 31; Conservative
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Location/Qualifiers
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Local Similarity 36.1%;
les 52; Conservative
                                                      Query Match 1.6%;
Best Local Similarity 36.1%;
Matches 52; Conservative
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/transl_table=11
/product="preproprotease"
/bxxef="prig490197"
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LTAQAAVRRAAADEPPEWNDFGV"
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Garvin,R.T. and James,E.
Froduction of active proteins containing cystine residues
Patent: EP 022279-A 5 20-MAY-1987;
Cangene Corporation
                                                                                                                                                               Streptomyces griseus
Eubacteria: Firmicutes; Actinomycetes; Streptomycetes;
Extraptomycetaceae; Streptomyces.
1 (bass 1 to 201)
Garvin, R.T. and James, E.
Production of active proteins containing cystine residues
Patent: EP 0222279-A 2 20-MAY-1987;
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/db_xref="PID:9490656"
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Pred. No. 4.16e-02;
35; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  46 others
                                                         S.griseus gene for preproprotease (partial). A10158
                                                                                                                                                                                                                                                                                                    /organism="Streptomyces griseus"
/db_xref="taxon:1911"
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Db 16103 CYYGMYSWCSYKMKYSRYCCGCCYSSSYCKSC 16134
                 1500 CCAGAGGCCTGGGGGCACCAGCCGGCGCAGGC 1469
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                                                                                                                                                     Streptomyces griseus.
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Local Similarity 36.1%;
les 52; Conservative
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/translation="MPHSPVSPAESPAPQPGRPRPVVSRRLLEGGAAVLGALALSASP
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66 c 51 g 22 t 46 others
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attificial sequence.
1 (bases 1 to 201)
Garvin.R.T. and James,E.
Production of active proteins containing cystine residues
Patent: EP 022279-A 6 20-MAY-1987;
Cangene Corporation
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Synthetic DNA for preproprotease leader & prochymosin.
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Pred. No. 4.16e-02;
35; Mismatches 57; Indels
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/db_xref="taxon:32630"
t 51 c 66 g
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

 $\rm n.a.$ - $\rm n.a.$ database search, using Smith-Waterman algorithm with gap extension penalties as well as gap opening penalties MPsrch_nna

Thu Dec 24 13:04:47 1998; MasPar time 5213.74 Seconds 659.468 Million cell updates/sec Run on:

Tabular output not generated.

Title:
Description:
Perfect Score:
N.A. Sequence:
Comp:

>US-08-951-733-13 (1-1920) from US08951733.seg (1 of 2) 1920

1 CACGCGTCCGGGCAGCGCTG.......CCAGGCCCGCCCTGCTGACG 1920 GTGCGCAGGCCGGCGGGACGACTGC

TABLE default Gap open 30; Gap extend 1 Scoring table:

Dbase 0; Query 0

Nmatch STD

2275026 seqs, 895388244 bases x.2 Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

embl-est55 Database: Database:

1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3 genbank-est107 5:gb_est107 10:gb_est14 11:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13 10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17 14:gb_est21 19:gb_est19 16:gb_est2 17:gb_est20 18:gb_est21 19:gb_est3 20:gb_est4 21:gb_est5 22:gb_est6 23:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss1 27:gb_gss2 28:gb_gss3 29:gb_gss4

Mean 11.357; Variance 2.736; scale 4.151 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ė l	00	46	41	34	27	10	07	07	90	05	90	05
	Pred. No	0.00e+00	1.27e-46	7.79e-41	9.33e-34	6.93e-27	2.10e-10	5.22e-07	5.22e-	6.33e-06	7.23e-05	6.33e-06	7.23e-05
	Description	zt08902.rl NCI_CGAP_GC	97SN1787 Rice Immature	97SN1787 Rice Immature	97SN1784 Rice Immature	97SN1784 Rice Immature	Homo sapiens ntcon6 co	Homo sapiens clone ntc	Homo sapiens clone ntc	CIT-HSP-2288C3.TF CIT-	yp24c08.rl Homo sapien	Homo sapiens ntcon6 co	Homo sapiens ntcon2 co
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	Query Match Length DB	389	252	252	247	247	099	1287	1287	317	400	099	2275
æ	Query	11.8	3.0	2.8	5.6	2.3	1.6	1.5	1.5	1.4	1.4	1.4	1.4
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## ALIGNMENTS

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llarity 8.7%;
Conservative 1
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Best Local Similarity 12.8%;
Matches 23; Conservative
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/organism="Oryza sativa"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
X/OID Directional CDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
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AA754459 92801165
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1 (bases 1 to 252)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Kim, W.T., Kim, W.T., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seg primer: Mi3 Reverse Primer.
Location/Qualifiers
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Email: myeun@sun20.asti.re.kr
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1 Similarity 99.1%;
229; Conservative
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XhoI; Directional cDNA library inserted into lambda ZAPII vector at 5'end with EcoRI and 3' end with Xho I site." /db_xref="taxon:4530" /clone="97SNI787" /clone="97SNI787" /fissue_type="Immature Seed Lambda ZAPII cDNA Library" /dev_ztage="5" anys after pollination" /lab.host="E. coli SOLR"
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AA754459 92801165
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/der_stage="5 days after pollination"
/lab_host="E. coli Solr"
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21 c 12 g 35 t 179 others
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Bubryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.

1 (bases 1 to 252)

1 (bases 1 to 252)

Mahn, B.H., Kim, N.T., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P.,
Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
Lee, M.C. and Eun, M.Y.
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National Inst. of Agri. Sci. and Tech, RDA
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel. 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: Ml3 Reverse Primer.
Location/Qualifiers
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/organism="Oryza sativa"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
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Pred. No. 7.79e-41;
105; Mismatches 85; Indels
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Pred. No. 1.27e-46;
88; Mismatches 69; Indels
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                                                                                                                                                                                                                                                                                              AA754458 247 bp mRNA EST 20-JAN-1998
SySNIYB4 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
CDNA Clone 97SNI784, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .247,
// Organism="Oryza sativa"
// Organism="Myang23"
// Outlivam="Wilyang23"
// Note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
// Note="vector at 5'end with EcoRI and 3' end with Xho I site."
// Ab_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_1975W1784"
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
a 16 c 21 g 34 t 169 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae: Viridiplantae; Charophyta/Embryophyta group; Embryophyta: Tracheophyta; seed plants; Magnoliophyta; Liliopsida; Poacles: Oryae.

1 (bases 1 to 247)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Nahm, B.H., Kim, W.T., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungqido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0301
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji.
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
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                                                                     80 WBVBNTKVDVGNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTM 139
                                                                                                                                           140 WCWBHYNTKCTASGWHTSTNYDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVSTTRA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 INTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBTAYCDYBHYBDRANHVDDTRCTNDRGYC 147
                  GIGIGGEGETCACCTGCCAGACCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTG 937
                                                                                                                                                                  TTSYBCHGNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMTWGTVNWBNVSGDWHY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 TBBWCCVRRVGTTTNNGKHNGRTTTWNDCSDNAHCRYTVBWYYARSKYGYGTBYYSWNVD 87
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Pred. No. 9.33e-34;
93; Mismatches 88;
                                                                                                                                                                                                                                      998 GGGGGCACCACGTCCTGGGACACGCC 1025
                                                                                                                                                                                                                 200 TRSYTCVRKYCVMWMTKKVVKKYHVVBB 227
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Best Local Similarity 13.0%;
Matches 27; Conservative
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97SN1784 Rice Immature Seed Lambda ZAPII CDNA Library Oryza sativa cDNA clone 97SN1784, mRNA sequence.
AA754458
92801164
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/organism="Oryza sativa"

/organism="Oryza sativa"

/organism="Oryza sativa"

/organism="Oryza sativa"

/orota="ve-cor" pBluescript SK(+); Site_1: EcoRI; Site_2:

XhoI; Directional cDNA library inserted into lambda ZAPII

/db_xref="taxon: 4530"

/clone="975N1784"

/clone="975N1784"

/clone="1b="Rice Immature Seed Lambda ZAPII cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Bibryophyta; Tracheophyta; seed plants; Magnollophyta; Liliopsida;
Poales; Poaceae; Oryza.

1 (bases 1 to 247)

Mahn, B.H., Kim, N.Y., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P.,
Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungqido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0301
Email: myeun@sun20.asti.re.kr
Submitted by Back Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: Mi3 Reverse Primer.
Location/Qualifiers
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                                                       207
                                                                                   302 AGCTGGTGGCCCGAGTGCTGCTGCTGCGAGCGGGGGGGGAAGAAGAACGTGCTGGCCT 361
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148 NYTASDNGTSATKRVTGYDKTDSDCGGGGWRKVTYGSSBYBRCGVNVMVRTTSMWTDKST
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Pred. No. 6.93e-27;
65; Mismatches 45; Indels
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/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
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                                                                                                                                                           208 KMBSMDMSRRSRVHYGRWMBNKKRGMSR 235
                                                                                                                                                                                            362 TCGGCTTCGCGCTGCTGGACGGGGCCCG 389
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Best Local Similarity 12.0%;
Matches 15; Conservative
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Homo.
Primates; Catarrhin; Hominidae; Homo.
Tripodiss. Ito 1287)
Tripodis. N. and Ragoussis, J.
Direct Submission
Submitted (12-DEC-1997) Division of Medical and Molecular Genetics, Guy's Hospital, 7th floor, Guy's Tower, London SEI 9RT, UK
                                                                                                                                                                                                                                              2 (bases 1 to 660)
Tripodis,N. and Ragoussis,J.
Direct Submission
Submitted (13-NOV-1997) Division of Medical and Molecular Genetics,
Guy's Hospital, 7th floor, Guy's Tower, London SEl 9RT, UK
Location/Qualifiers
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              p mRNA EST 22-DEC-1997 contig mRNA, partial sequence.
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HOMO Sapiens clone ntcon9 mRNA, partial sequence, mRNA sequence.
AF038250
92815880
                                                                                                                                                                                                                                                                                                                                                                                                             /mar-criticans contig"
/tissue_type="fetal brain; fetal liver; adult muscle"
/tote="similar to CutA"
/note="similar to CutA"
a 161 c 173 g 109 t 55 others
                                                                                                      Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                    1 (bases 1 to 660)
Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately
centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
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Pred. No. 2.10e-10;
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Pred. No. 5.22e-07;
29; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 WSSRCCYRSYGMYHYYYCYYKKCDMSCTTSKSRWYKSKRSWCDCD 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //clone="ntcon9"
//dev_stage="fetal"
/tissue_type="brain; liver"
/note="similar to HSRP20"
219 c 393 g 361 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31; Mismatches
                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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      Homo sapiens ntcon6 co
AF034177
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Local Similarity 15.6%;
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Best Local Similarity 29.1%;
Matches 23; Conservative
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalla; Eutherla; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 1287)
1 (bases 1 to 1287)
1 ripodis, N. and Ragoussis, J.

Direct Submission
Submitted (12-DEC-1997) Division of Medical and Molecular Genetics, Guy's Hospital, 7th floor, Guy's Tower, London SEI 9RT, UK
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( bases 1 to 317)
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                         AF038250 1287 bp mRNA EST 29-JAN-1998
Homo sapiens clone ntcon9 mRNA, partial sequence, mRNA sequence.
AF038250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 DCBTGGGDTBSHBVCMCBCBANADGATBATCGKVGGVBGASTCMTHYNCCDCKTCGSAGV 460
                       407 GDTBSHBVCMCBCBANADGATBATCGKVGGVBGASTCMTHYNCCDCKTCGSAGVTVNHHD 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIT-HSP-2288C3.TF CIT-HSP Homo sapiens genomic clone 2288C3, AQO08007
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Pred. No. 5.22e-07;
29; Mismatches 19; Indels
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/tissue_type="brain; liver"
/note="similar to HSRP20"
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Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db.xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/clone="ntcon9"
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                                                                                                                   |: ::: : | | :||||
287 TGTCCTGCCTGAAGGAGCT 305
                                                                                       461 TVNHHDWSMAGGAARAGCT 479
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Best Local Similarity 23.8%;
Matches 15; Conservative
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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1. .400
/organism="Homo sapiens"
                                     /clone="188366'
. 123 c 11
                                                                                                         1.48;
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Best Local Similarity 23.6%;
Matches 13; Conservative
                                                                                                                                           39; Conservative
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Matches 39; Conser
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Tel: 301 838 0200
Tel: 301 838 0200
Emai: adadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
ttp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13-21;
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Osteichthyes;
Beuterostoomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 400)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Rucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
High quality sequence stops: 363
Source: INAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (life@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human clone-188366 library-Soares breast 3NbHBst vector=pT7T3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                  Location/Qualifiers

1. 317
/organism="Homo sapiens"
//note="Wector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                Length 317;
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                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 6.33e-06;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                75
                                                                                                                                                                                                                                             /db_xref-"taxon:9606"
                                                                                                                                                                                                                                                           /clone="2288C3"
/clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                             /cell_type="Sperm"
92 c 91 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-Merck EST Project Unpublished (1995)
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                                                                                                                                                                                                                                                                                             /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.4%;
Best Local Similarity 86.5%;
Matches 32; Conservative
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ACCESSION
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Direct Submission State of Medical and Molecular Genetics, Submitted (13-NOV-1997) Division of Medical and Molecular Genetics, Guy's Hospital, 7th floor, Guy's Tower, London SE1 9RT, UK Location/Qualifiers
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Homo sapiens ntcon2 contig mRNA, partial sequence, mRNA sequence.
AF034173
92707735
                                                                                                                                                                                                                                                                                               AF034177 660 bp mRNA EST 22-DEC-1997
Homo sapiens ntcon6 contig mRNA, partial sequence, mRNA sequence.
AF034177
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1 (Dases 1 to 2275)

Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 brain; fetal liver; adult muscle"
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Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately
centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                           Gaps
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                                                                                                                                                                                               128 TGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGCGTG 180
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                                                                           Length 400;
     10 others
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                                                                      Score 26; DB 16; Length 400
Pred. No. 7.23e-05;
0; Mismatches 14; Indels
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  79
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/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="ntcon6 contig"
/tissue_type="fetal bra
/note="similar to CutA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
2 (bases 1 to 660)
Tripodis, N. and Ragoussis, J.
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113 g
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BASE COUNT
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                                                                                                                                                             ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI171394 143 bp mRNA EST 07-0CT-1998 EST217350 Normalized rat muscle, Bento Soares Rattus sp. cDNA clone RMUBK19 3' end, mRNA sequence.
2 (bases 1 to 2275)
Tripodis.N. and Ragoussis,J.
Direct Submission
Submitted (13.NOV-1997) Division of Medical and Molecular Genetics,
Guy's Hospital, 7th floor, Guy's Tower, London SEl 9RT, UK
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 143)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
Rerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                             1895 CGATGCTGCTCTGCTTCCGACAGCTCCCGCAGCTGCACCTCTTCAAGTGCTGT 1836
                                                                                                                                                                                                                                                                                                                                                                                       1481 YKRWKRRKGRRKRWIGMYKRMYRAMMAMCAMMACWWYYWKMRGMKKCWKYRKYKKYTST 1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: muscle; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI" /db_xref="taxon:10118"
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                                                                                                                                                                                                                                                                                                                  Length 2275;
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Pred. No. 7.73e-04;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                   149 others
                                                                                                                                                                                                                                                                                                                  Score 26; DB 11; Length 227
Pred. No. 7.23e-05;
55; Mismatches 38; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="fp21.3"
/clone="ntcon2"
/tissue_type="liver; brain"
/dev_stage="fetus"
/note="similar to Br140"
a 619 c 470 g 599 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seg primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene Index
Unpublished (1998)
Other_ESTS: TC52270
Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                    Query Match 1.4%;
Best Local Similarity 8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.3%;
Best Local Similarity 76.6%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                       Conservative
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93711434
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                   AUTHORS
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   REFERENCE
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Colleman, T.R., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Rozak, D.L., Runsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
infox (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
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ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):174439"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 TGCCGCGCGCCTCCCCGCTGCCGAGCCGTGCGCTGCGCGAGCCACTACCGCGAGG 127
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                                                                                                       AA386387 181 bp mRNA EST 22-APR-19
EST81369 Prostate gland I Homo sapiens CDNA 5' end similar (
proly1 4 hydroxylase, beta subunit/protein disulfide isomerase/thyroid hormone-binding protein, mRNA sequence. AA386387
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Bioinformatics
The Institute for Genomic Research
9712 medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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                                   57
103 GGGAGCGCACGGCACCGCAGCGCGCGCGCATCGCGGGGGTG
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/clone_lib="Prostate gland
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Best Local Similarity 70.0%;
Matches 42; Conservative
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4 GGGAGCGCATGGGCCGGCTGCGGGCTCGCGCCGCTGCTG 50

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AA855630 187 bp mRNA EST 06-MAR-1998 vw68h11.rl Stratagene mouse heart (#937316) Mus musculus cDNA clone 1260165 5' similar to TR:Q99960 Q99960 PLAKOPHILIN 2A. [1] ;, mRNA
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 187)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
65 c 70 g 23 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 GGCTGGCGGCAGCAGCGGCGGCGACCCGGCGGC 139
                                                                                                                                                                                                                                 Waterston, R.
The WashU-HHMI Mouse EST Project
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1.3%;
Best Local Similarity 85.7%;
Matches 30; Conservative
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                                                                                                                        Mus musculus
                                                                                                           house mouse.
                                                   sequence.
AA855630
g2943168
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15
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SOURCE
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JOURNAL
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AUTHORS
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RESULT
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169 GGCTGGCGGCTGGTGCAGCGGGGACCCGGCGGC 203

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Search completed: Thu Dec 24 14:55:23 1998 Job time : 6636 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

 $\rm n.a.$  -  $\rm n.a.$  database search, using Smith-Waterman algorithm with gap extension penalties as well as gap opening penalties MPsrch_nna

Thu Dec 24 14:55:42 1998; MasPar time 578.35 Seconds 451.671 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-951-733-13 (1-1920) from US08951733.seq (1 of 2) 1920 Description: Perfect Score: N.A. Sequence:

1 CACGCGTCCGGGCAGCGCTG.......CCAGGCCCGCCCTGCTGACG 1920 GTGCGCAGGCCCGTCGCGACACTGC

TABLE default Gap open 30; Gap extend 1 Scoring table:

Dbase 0; Query 0 STD Nmatch

188442 seqs, 68026449 bases x Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

n-geneseq32 Database:

| Spart | 2:part | 3:part | 4:part | 5:part | 5:part | 7:part | 5:part | 5:part | 5:part | 5:part | 1:part | 1:

Variance 6.325; scale 1.481 Mean 9.368; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

 Score	Query Match	Ouery Match Length DB	DB	Ð	Description	Pred. No.
45	2.3	91	. 6	051746	Oligonucleotide probe	3.546-10
45	2.3	91	σ	051746	Oligonucleotide probe	3.54e-10
43	2.2	204	Н	N81164	Base substituted E.co	3.86e-09
40	2.1	114	12	070466	Generic DNA sequence	1.32e-07
39	7.0	114	12	970469	Generic DNA sequence	4.21e-07
38	2.0	114	12	070468	Generic DNA sequence	1.33e-06
38	7.0	114	12	070467	Generic DNA sequence	1.33e-06
38	2.0	114	12	070468	Generic DNA sequence	1.33e-06
38	2.0	114	12	070465	Generic DNA sequence	1.33e-06
39	2.0	178	32	T76405	Human endothelin-1 an	4.21e-07
38	2.0	204	Н	N81164	Base substituted E.co	1.33e-06
36	1.9	114	17	070467	Generic DNA sequence	1.31e-05

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6 cggcgssvhsyyvvhvvshhhsvhhvvhhvhvvhvvhhvhhvhyhvyvsv 60

RESULT

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74 4 12 6 7 7 12 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	.38; 1Ve
14 36 1.9 114 12 15 36 1.9 114 12 16 36 1.9 114 12 18 35 1.8 162 32 18 162 32 22 35 1.8 162 32 23 35 1.8 172 32 24 35 1.8 172 32 25 32 1.7 114 12 29 32 1.7 114 12 29 32 1.7 114 12 29 32 1.7 114 12 31 30 1.6 100 32 33 31 1.6 100 32 34 30 1.6 114 12 35 38 30 1.6 114 12 36 31 1.6 100 32 37 30 1.6 114 12 38 30 1.6 114 12 39 30 1.6 114 12 39 30 1.6 114 12 39 30 1.6 128 32 44 29 1.5 168 32 44 29 1.5 168 32 44 29 1.5 168 32 44 29 1.5 168 32 45 29 1.5 168 32 46 29 1.5 168 32 47 30 1.6 114 12 38 30 1.6 201 2 41 30 1.6 201 2 41 30 1.6 201 2 41 30 1.6 201 2 42 29 1.5 168 32 44 29 1.5 168 32 45 29 1.5 168 32 46 29 1.5 168 32 47 48 29 1.5 168 32 48 29 1.5 168 32 49 29 1.5 168 32 40 29 1.5 168 32 41 30 1.6 114 12 39 30 1.6 114 12 39 30 1.6 128 32 39 30 1.6 201 2 41 30 1.6 128 32 42 484 - 1992; US-889551. 44 29 1.5 189 551. 44 29 1.5 189 561. 45 29 1.5 189 561. 46 29 1.5 189 561. 48 WPI: 93-378844/48. 49 199-378844/48. 40 199-378844/48. 40 199-378844/48. 40 199-378844/48. 40 199-378844/48. 40 199-378844/48. 40 199-378844/48. 40 199-378844/48. 41 299 1.5 299 1.5 205-388561. 42 29 1.5 205-388561. 43 29 1.5 205-388561. 44 29 1.5 205-388561. 45 29 1.5 205-388561. 46 20 1.0 20 20 20 20 20 20 20 20 20 20 20 20 20	larity 7. Conservati
standard; cleentide pires of cle	imila 4;
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Best Local Similarity 20.9%;
Matches 31; Conservative
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01-FEB-1994;
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Introducing random point mutations into nucleic acods --
Introducing random point mutations into nucleic acods --
by prepn of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.
Disclosure; p; English.
Exandom point mutations were introduced into the alpha fragment of
E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to
it to generate a popn of DNA molecules which terminate at all
possible nucleotide positions within a specified ragion. The
variable 3' ends generated in this way are used as primers for
reverse transcriptase. Nucleotides are misincorporated by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 tccggcgssvhsyyvvhvvshhhsvhhvvhvvhhvvhvvhhvhhvhyhvyvsvct 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                              MK14
but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-1990 (first entry) assess by tragment. Base substituted E.coll beta-galactosidase alpha-fragment. E.coll beta galactosidase alpha-fragment; base substitutions; ss. Escherichia coll.
                                                                                                                                                                                                                                                                                                          - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERL OX.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
WPI: 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59;
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                    31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                        New oligo:nucleotide probes specific for Mycobacteria – use detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 9; Lv
Pred. No. 3.54e-10;
45; Mismatches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 3
N81164 standard; DNA; 204 BP.
N81164;
  ВР
                                                                                                                                                                                           24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 11.9%;
Matches 7: Connection
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Q51746 standard; cDNA; 91
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WPI; 93-378844/48.
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30-MAR-1988; 105163.
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                                                                                                                                                     EP-571911-A.
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ID N8
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NAME OF THE PART O
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Score 43; DB 1; Length 204;

2.28;

Query Match

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Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins promprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English.

Disclosure; Page 35; 255pp; English.

Comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English.

Coffee is a generic DNA Sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)1(TGC)(NNB)10(TGC)2(NNB)4Z(NNB)8(TGC)(NNB) 0.9Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specific peptides generated by these generic sequences are shown in R65151-54. TSARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a contrained so that the expressed peptide contains 2 or 4 cysteine residues confer some degree of conformational rigidity to the peptides. They can also replace to the function of macromolecules, eg. residues confer some degree of conformational rigidity to the peptides. The TSARs or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal cont, radiolsotope, peptide, toxin or enzyme, to the specific target or complex methods of hybridoma formation or in vivo antibody production.

Complex methods of hybridoma formation or in vivo antibody production.

Complex methods of hybridoma formation or in vivo antibody production.

Complex methods of hybridoma formation or in vivo antibody production.
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                                                                                                                     bcyrraggnyccccggggywccgagcycgaayycdchvgccgymrttthhyrrmrbnvyrd 104
                                                                                                                                                                                                                                                                        105 ynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnneneecbnnhvehnv 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G5-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR-9 petide library.
TSAR, totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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Pred. No. 1.32e-07;
32; Mismatches 70; Indels
Pred. No. 3.86e-09;
57; Mismatches 60; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                      165 hbnnhrnwayvrhdarrddvhccvchcc 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UNNC-) UNIV NORTH CAROLINA.
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llarity 8.9%;
Conservative.
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WPI; 94-279739/34.
P-PSDB; R65152.
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Matches 10; Conser
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(first entry)

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JT 6
Q70468 standard; DNA; 114
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                                                              070468;
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PAR WPI: 94-27939343.

Identifying proteins or peptide(s) which bind a ligand - by careening a recombinant vector library expressing fusion proteins recening a recombinant vector library expressing fusion proteins a recombinant vector library expressing fusion proteins promprising a binding domain and an effector domain proteins page 35; 255pp; English.

CC 070469 is a generic DNA sequence used to generate random TSAR peptide CT his generic formula can be represented as follows: X(TGC)(NNB)10-CC (TGC)(NNB)2(ZNNB)2(TGC)(NNB)14(TGC)) X and Y are flanking restriction sites (X is not the same as Y) that are not specific peptides restricted presence generic sequences are shown in 070465-68. Other specific peptides concatenated by these generic sequences are shown in R65150-54. TSARs are generated by these generic sequences are shown in R65150-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically a further comprise a linker peptide between the 2 domains. Contains 2 or 4 cysteine residues positioned in, or flanking, the contoins 2 or 4 cysteine residues positioned in, or flanking, the contoins and office of a TSAR binding domain can be used in vivo to deliver a chemically or belobogically active molety, eq. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eq. monoclonal or publication or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid represent and reperior and reperior and reperior and reperior and reperiors.
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Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                             GTGCGCCCCTGGGCCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTC
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                                                                                                                                                                                                                                                                                                            sequence represents '2'; Z can be 5,9 or 12 nucleotides (see
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                                                                                       CGCGCGCTGGTGCCCAGTGCCTGGTGCGTGCCTGGGACGCACGGCCGC 259
                                                          63 banbanbanbanbanbanbanbtgcanbanbanbanbanbanbanbanb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 114;
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32; Mismatches 71; Indels
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comments)"
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Q70469 standard; DNA; 114 BP
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UTNC-) UNIV NORTH CAROLINA.
FOWIKES DM, RAY BK;
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Matches 8; Conser
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Presenting a recombinant vector library expressing fusion proteins

PT comprising a blunding domain and an effector domain

PT screening a recombinant vector library expressing fusion proteins

PT comprising a blunding domain and an effector domain

Disclosure; Page 35; 255pp; English.

CC GMPG is a generic DNA sequence used to generate random TSAR (Totally

CS Synthetic Affility Reagents) peptides. This generic formula can also be

represented as follows: X(NNB)11(TC)(NNB)52(NNB)7(TG)(NNB)10Y. X

and Y are flanking restriction sites (X is not the same as Y) that are

CC offer specified further. Other generic sequences are shown in 707466-68.

CC other specific peptides generated by these generic sequences are shown in 685151-54. TSARs are concatenated heterofunctional proteins or peptides.

CC offer specified and a second effector peptide portion that is affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker of fainity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker of fainity for a ligand and a second effector peptide seals of seasigned so that the expressed peptide contains? The Olygonucleotides are also designed so that the expressed peptide contains 2 or 4 cyteine residues positioned in, or flanking, the unpredicted or variant residues. Therefore confer some degree of conformational rigidity to the peptides. The TSARs or comprise, peptide, toxin or enzyme, to the specific target or on the conformation or enzyme, to the specific target or on the conformation or enzyme, to the specific target or on the conformation of macromolecules, eq.

Cor compiex methods of hybridoma formation or in vivo antibody

CD concepted and rapid detection in a screening process.

Sequence 114 BP; 0 A; 2 C; 2 C; 2 C; 2 C;
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Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; reffector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                 /uote= "this sequence represents '2'; 2 sequence of 6, 9 or 12 nucleotides (see comments)"
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34; Mismatches 73
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
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5; Conservative
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WPI; 94-279739/34.
P-PSDB; R65154.
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Best Local Similarity
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01-FEB-1994;
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Trends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss. Synthetic.
                                                                                                              Ø
                                                                              55..60
/*tag= 1
http://with.assequence represents '2'; Z can be
sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 12; ]
Pred. No. 1.33e-06;
                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 55..60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 8
Q70468 standard; DNA; 114 BP.
Q70468;
                                                                                                                                                                                                                                     31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Kay BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.0%;
llarity 4.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-1995 (first entry)
                                                                                                                                           comments)"
                                                                                                                                                                                      U00977.
US-013416.
US-176500.
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Best Local Similarity
                                                                                                                                                                                                                                                                                  WPI; 94-279739/34.
P-PSDB; R65153.
                                                                                                                                                                                                                    30-DEC-1993;
31-JAN-1994;
                                                                                                                                                                                       01-FEB-1994;
01-FEB-1993;
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                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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Synthetic Affinity Reagents) peptides. This generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(MNB)11(TGC)(NNB)5(X) (NNB)5(X) (NRD)10(X) X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in 070466-68. Other specific peptides generated by these generic sequences are shown in 65151-54. TSARs are concatenated by these generic sequences are shown in 65151-54. TSARs are concatenated by these generic sequences are shown in 65151-54. TSARs are concatenated by these generic sequences are shown in 65151-54. TSARs are concatenated by these generic sequences are shown in 65151-54. TSARs are concatenated by these generic sequences are shown in 65151-54. TSARs are concatenated by these generic sequences are shown in 65151-54. TSARs are concatenated between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compans. comprising a TSAR binding domain can be used in vivo to radioisotope, peptide, toxin or enzyme, to the specific target or on the conformation of maching and also replace the function of macromolecules, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1542 CTTGGTGTTCCTGAGGAAGCGGCGTTCGTTGTGCCTGGAGCCCCAGAGGCCTGGGGGCAC 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bnabanbanbanbanbanbanbanbanbanbtgcanbanbanbanbanbanbananan 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure; Page 35; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ๙
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 banbanbanbanbanbanbtgcanbanbanbanbanbanbanbanbanb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 114;
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//note= "this sequence represents 'Z'; Z
sequence of 6, 9 or 12 nucleotides (see
comments)"
/note= "this sequence represents 'Z'; Z sequence of 6, 9 or 12 nucleotides (see comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.33e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                л. 9
Q70465 standard; DNA; 114 BP.
                                                                                                                                                                                                         01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UNC-) UNIV NORTH CAROLINA.
FOWLKES DM, RAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.0%;
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01-FEB-1994; U00977.
01-FEB-1993; US-0134
                                                                                                                                                                            T00977
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                                                                                                                                                                                                                                                                                                                                                                               WPI; 94-279739/34.
P-PSDB; R65154.
                                                                                                                                            18-AUG-1994.
01-FEB-1994;
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                                                                                                                                                                                                                                                                                                                                                                             NAME OF THE PART O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1527 GAAGCGGCGTTCGTTGTGCCTGGAGCCCCAGAGGCCTGGGGGGCACCAGCCGGCGCAGGCA 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         method for treating airway disease in a subject has been produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma, chronic obstructive pulmonary disease, bronchitis and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1467 GGCCCGCACGAAGCCGTACACCTGCCAGGGGCTGCTGTGCTGGCGGAGCAGC 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asthma; airway epithelium; adenosine free; cystic fibrosis; chronic obstructive pulmonary disease; bronchitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 12; Length 114
Pred. No. 1.33e-06;
34; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-1997 (first entry)
Human endothelin-1 antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 38; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T76405 standard; DNA; 178 BP.
                                (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995; US-474497.
(UYEC-) UNIV EAST CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       larity 4.5%;
Conservative
                                                                                        P-PSDB; R65150 and R65151.
US-176500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metzger WJ, Nyce JW;
WPI; 97-051871/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-1996.
06-JUN-1996; U09306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                     WPI; 94-279739/34
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                                                        Fowlkes DM
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WPI: 88-27997740.

Throducing random point mutations into nucleic acods -
by prepo of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.

Disclosure; p; English.

Exadom point mutations were introduced into the alpha fragment of
E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to
it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for variable 3' ends generated in this way are used as primers for temperateses and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which courred singularly in any given mutant.

See also P80575.
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                                                                                                                                                                                                                                                                                                                                 80 hvgccgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvyb 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 AAGCCGCCGGGTCCCCGCGCTGCACCAGCCGCCAGCCCTGGGGCCCCCAGGCGCCGCACGA 146
                                                                                                                                                                                                                                                                                                cbbgccbcbbccbgcbgcbgbgbbbbtcbtgbgcbbbtbbtccbttctgbbbbbbbgggbt 164
airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstrint in patients with hyper-reactive airways. Sequence 178 BP; 0 A; 52 C; 46 G; 32 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
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Lehtovaara P. Knowles J, Koivula A, Bamford J, Reinikainen T;
                                                                                                                                                                             Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 204;
                                                                                                                                                                             Score 39; DB 32; Length 178
Pred. No. 4.21e-07;
34; Mismatches 17; Indels
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/function=multiple cloning site
187..204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N81164 standard; DNA; 204 BP.
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                                                                                                                                                                          2.0%;
larity 30.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.0%;
Best Local Similarity 16.1%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N81164;
08-NOV-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UT 12
Q70467 standard; DNA; 114
Q70467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                             165 cbbbbbcctcccg 177
                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-1988; 105163
03-APR-1987; US-0348
                                                                                                                                                                                                        Best Local Similarity
Matches 22; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                                                                                                                                                                Query Match
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misc_feature
                                                                                                                                                                         Fowlkes DM
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Tentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PT screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure; Page 35; 255pp; English.

CQ70467 is a generic DNA Sequence used to generate random TSAR (Totally

CQ 770467 is a generic DNA Sequence seed to generate formula can also be

represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)1X

CG and Y are flanking restriction sites (X is not the same as Y) that are

CC other specified further. Other generic sequences are shown in Q70466-68.

COTHER SPECIAL SPECIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 CICCCIGCIGCGCAGCCACIACCGCGAGGIGCIGCCGCIGGCCACGIICGIGCGGCGCCI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generic DNA sequence to generate a random TSAR peptide library.

TSAR; totally synthetic affinity reagent; synthetic; binding domain, effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.

Synthetic.

Location/Qualifiers
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/note= "this sequence represents 'z'; Z can be
sequence of 6, 9 or 12 nucleotides (see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        direct and rapid detection in a screening process Sequence 114 BP; 0 A; 2 C; 2 G; 2 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 12; I
Pred. No. 1.31e-05;
34; Mismatches 74;
                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 13
Q70470 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                           (UYNC-) UNIV NORTH CAROLINA. Fowlkes DM, Kay BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.9%;
3.6%;
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10-APR-1995 (first entry)
 (first entry)
                                                                                                                                                                                         comments)
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                                                                                                                                                                                                                                                           US-013416.
US-176500.
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30-DEC-1993; US-176500
31-JAN-1994; US-189331
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Best Local Similarity
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05-APR-1995
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                                                                                    Synthetic.
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Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PT screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure; Page 36; 255pp; English.

C10470 is a generic DNA Sequence used to generate random TSAR (Totally

C2070470 is a generic DNA Sequence used to generate random TSAR (Totally

C2070470 is a generic DNA Sequence used to generate formula can also be

C2070470 is a generic DNA Sequence used to generate to the same

C2070470 is a generic DNA Sequence used to stress (TAND) (CAC) (NND) 82 (NND
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Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 bnnbnnbnnbnnbnnbcacnnbnnbnnbnnbnnbnnbnnbcaccacnnb 114
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//*tag= a
//note= "this sequence represents 'Z'; Z
equence of 6, 9 or 12 nucleotides (see
comments) "
                                                                     /note= "encoded by Z (see comments)"
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Best Local Similarity 9.8%;
Matches 11; Conservative
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US-176500.
US-189331.
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P-PSDB; R58378.
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01-FEB-1994; U
01-FEB-1993; U
30-DEC-1993; U
31-JAN-1994; U
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31-JAN-1994;
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05-APR-1995
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Territy woolly and woolly.

Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PT screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure, Page 35; 255pp; English.

COMPAGE is a generic DNA Sequence used to generate random TSAR (Totally

COMPAGE is a generic DNA Sequence used to generate random TSAR (Totally

COMPAGE as follows: X(NNB)6(TGC)(NNB)12(NNB)14(TGC)(NNB)3Y. X

and Y are flanking restriction sites (X is not the same as Y) that are

COMPAGE as follows: X(NNB)6(TGC)(NNB)112(NNB)14(TGC)(NNB)3Y. X

and Y are flanking restriction sites (X is not the same as Y) that are

COMPAGE as generated by these generic sequences are shown in

COMPAGE as a ligand and a second effector peptide portion that is:

COMPAGE AS A ligand and a second effector peptide portion that is:

COMPAGE AS A ligand and a second effector peptide portion that is:

COMPAGE AS A lightly active. They may further comprise a linker

COMPAGE AS A lightly active. They may further comprise a linker

COMPAGE AS A lightly active and a lightly to the peptides. The TSARS

COMPAGE AS A lightly active moiety, eq. metal ion,

COMPAGE AS A LIBRARY AS A LIBRARY ACTIVE MOIETY, eq. metal ion,

COMPAGE AS A LIBRARY AS A 
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070469 is a generic DNA sequence used to generate random TSAR peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 GCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCTGCTGCTGCCACCACTACCGCGAGGT 128
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ISAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
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//note= "this sequence represents 'Z'; Z can be a
sequence of 6,9 or 12 nucleotides (see
comments)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 GCTGCCGCTGGCCACTTCGTGCGGCCCCTGGGGCCCCAGGGCTGGCGGCTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 12; Length 114,
Pred. No. 1.31e-05;
33; Mismatches 74; Indels
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070469;
070469;
07-APR-1995 (first entry)
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31-JAN-1994; US-189331.
(UINC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
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Best Local Similarity 4.5%;
Matches 5; Conservative
                                            R65150 and R65151
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01-FEB-1994; U00977.
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contains 2 or 4 cystein residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compens. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid
This generic formula can be represented as follows: X(TGC)(NNB)10-
(TGC)(NNB)2(ZTGC)(NNB)14(TGC)Y. X and Y are flanking restriction
sites (X is not the same as Y) that are not specified further. This
sequence generates peptides that are cloverleaf in structure. Other
generic sequences are shown in Q70465-68. Other specific peptides
generated by these generic sequences are shown in R65150-54. TSARs are
concatenated heterofunctional proteins or peptides, comprising at least
two functional regions - a binding domain with affinity for a ligand and
a second effector peptide portion that is chemically or biologically
active. They may further comprise a linker peptide between the 2 domains.
The oligonucleotides are also designed so that the expressed peptide
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Pred. No. 1.31e-05;
31; Mismatches 74; Indels
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C;
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Best Local Similarity
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Search completed: Thu Dec 24 15:06:48 1998 Job time : 666 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

 $\rm n.\,a.$  -  $\rm n.\,a.$  database search, using Smith-Waterman algorithm with gap extension penalties as well as gap opening penalties MPsrch_nna

Thu Dec 24 15:10:17 1998; MasPar time 3273.33 Seconds 628.529 Million cell updates/sec Run on:

not generated. Tabular output

>US-08-951-733-13 (1-1920) from US08951733.seq (1 of 1920

1 CACGCGTCCGGGCAGCGCTG.......CCACGCCCGCCCTGCTGACG 1920 GTGCGCAGGCCCGTCGCGAC......GGTCCGGGCGGGACGACTGC Title: Description: Perfect Score: N.A. Sequence: Comp:

TABLE default Gap open 30; Gap extend 1 Scoring table:

Dbase 0; Query 0 Nmatch STD

1665728 segs, 535777091 bases x 2 Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

n-pending Database:

1:P9 2:U6000 3:U6001 4:U6002 5:U6003 6:U6004 7:U6005 8:U6006 9:U6007 10:U6008 11:U7 12:U80 13:U81 14:U82 15:U83 16:U84 17:U84B 18:U85 19:U86 20:U87 21:U88 23:U90A 24:U90B 25:U91 26:NEWP 27:NEWU6 28:NEWU9

Mean 10.626; Variance 4.576; scale 2.322 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00		
Description	Sequence 13, Applicati	Sequence 19, Applicati	1, A	4	_		٦		Sequence 35, Applicati		173	Sequence 6, Applicatio	Sequence 1, Applicatio	Sequence 36, Applicati	Sequence 52, Applicati
А	US-08-951-	US-08-951-	US-08-911-	US-08-912-	US-08-911-	US-08-912-	us-09-052-	US-08-854-	US-09-026-	US-08-854-	US-08-851-	US-08-912-	US-09-042-	US-09-026-	US-08-911-
BB	22	22	22	22	22	22	24	21	23	21	21	22	23	23	22
Query Match Length DB	2848	3798	7029	3822	3855	4015	4015	4015	4023	4029	4029	4200	3496	3346	535
Query	100.0	100.0	9.66	99.4	99.4	99.4	99.4	99.4	99.3	83.1	83.1	78.0	23.6	14.6	13.5
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U	32	68	٠		-08-56	74	.26e-3
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US-08-951-733-13 STANDARD; DNA; UNC; 2848 BP.

Sequence 13, Application US/08951733
Sequence 13, Application US/08951733
GENERAL INFORMATION:
APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: NOVEL GENES ENCODING TELOMERASE PROTEINS
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: CA

CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,733
FILING DATE: 16-0CT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/873,039
FILING DATE: 11-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,189
FILING DATE: 11-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REFERENCE/DOCKET NUMBER: 34,688
REFERENCE/DOCKET NUMBER: 34,688
TELECOMMUNICATION NUMBER: A-433B
TELECOMMUNICATION NUMBER: A-433B
TELECOMMUNICATION NUMBER: A-433B COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 

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                                                         Length 2848;
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                                                        DB 22;
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                                                        Score 1920; DB 2
Pred. No. 0.00e+(
0; Mismatches
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TELEFAX: (805) 499-8011
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2848 base pairs
                                             978
                      TYPE: nucleic acid
STRANDEDNESS: single
                                                        Query Match
Best Local Similarity 100.0%;
Matches 1920; Conservative
                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE 2848 BP; 437 A;
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BP 3798 UNC; DNA; STANDARD; 540

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901 900 961

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AGGCGTGCCCCTGAGCCGGAGCGGACGCCCTTGGCAGGGTCCTGGGCCCAC
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SEQUENCE 3798 BP; 613 A; 1310 C; 1213 G; 662 T; 0 OTHER
                                                                                                                                                                                 Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1920; DB 22;
Pred. No. 0.00e+00;
0; Mismatches 0;
                                                                                                                                      COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elbpy disk
COMPUTER: Elbpy disk
COMPUTER: Elb PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,733
FILING DATE: 16-CCT-1997
CLASSIFICATION NUMBER: US 08/873,039
FILING DATE: 11-JUN-1997
PRIOR APPLICATION NUMBER: US 08/873,139
FILING DATE: 11-JUN-1997
PRIOR APPLICATION NUMBER: US 08/751,189
FILING DATE: 15-NOV-1996
ATTORNEY AGENT INFORMATION:
        Sequence 19, Application US/08951733
Sequence 19, Application US/08951733
GENERAL INFORMATION:
APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: NOVEL GENES EN
                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: A-433B TELECOMMUNICATION INFORMATION:
                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: CA
                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (805) 447-6504
TELEFAX: (805) 499-8011
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 3798 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                NAME: Oleski, Nancy A. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 1920; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
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                                                                                                                                ZIP: 91320-1789
                                                                                                                         USA
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MOLECULE TYPE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                               Query Match 99.6%;
Best Local Similarity 99.8%;
Matches 1915; Conservative
                                                                                                                                                                                                                                                 ATURE:
NAME/KEY: CDS
782.4177
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FILING
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1442 FGGCAGGTGTACGGCTTCGTGCGGGCCTGCGCGCCGGCTGGTGCCCCCAGGCCTCTGG 1501
                  1441 TGGCAGGTGTACGGCTTCGTGCGGGCCTGCCTGCGCGGCTGGTGCCCCCAGGCCTCTGG 1500
                                                                                                           TGGCTGCGCAGGAGCCCAGGGGTTGGCTGTGTTTCCGGCCGCAGAGCACCGTCTGCGTGAG 1681
                                                                                                                                              GAGATCCTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCCAGG 1741
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                                                                                                                                                                                                                    GGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGG
                                                                       AAGCATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCT
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Sequence 1, Application US/08911312
Sequence 1, Application US/08911312
GENERAL INFORMATION
APPLICANT: Cech, Thomas R.
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Moxin, Greeg B.
APPLICANT: Moxin, Greeg B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase
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                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
COUNTRY: USA
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CLASSIFICATION: 336
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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US-08-911-312-1 STANDARD; DNA; UNC; 7029
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FILING DATE: 14-AUG-1997
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Townsend
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6
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OTHER INFORMATION: /product= "human telomerase reverse OTHER INFORMATION: transcriptase (hTRT)"

OTHER INFORMATION: /note= "cDNA contained in plasmid OTHER INFORMATION: pGRN121"

SEQUENCE 7029 BP; 1416 A; 2122 C; 2051 G; 1440 T; 0 OTHER.
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                                                                                                                                                                                                                                                              NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFENCE/DOCKET NUMBER: 015389-002500US
TELEPHONE: (415,576-0200
TELEPHONE: (415,576-0200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Pred. No. 0.00e+00;
0; Mismatches 3;
                                  PRICE APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
US 08/851,843
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GCATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTG 1622
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                                      TGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACACTTGAAGAGGGTGCAGCTGCG
                                                                                                                     TITCITITATGICACGGAGACCACGITICAAAAGAACAGGCICITITICIACCGGAAGAG
                         GCTGCGCAGGAGCCCAGGGGTTGGCTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGA
                                                                        GATCCTGGCCAAGTTCCTGCACTGGTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC
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Sequence 4, Application US/08912951
Sequence 4, Application US/08912951
Sequence 4, Application US/08912951
Sequence A, Application US/08912951
Sequence APPLICANT: Cech, Thomas R. APPLICANT: Lingner, Joachim APPLICANT: Chapman, Karen B. APPLICANT: Morin, Gregg B. APPLICANT: Morin, Gregg B. APPLICANT: Andrews, William H. TILLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIA TITLE OF INVENTION: THERAPEUTIC METHODS
UWMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crew
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STREET: Two Embarcadero Center, 8th Floor
CIIY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                        US-08-912-951-4 STANDARD; DNA; UNC; 3855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 06-MAY-1997
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FILING DATE: 25-APR-1997
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APPLICATION NUMBER: US 08
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-1997
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APPLICATION NUMBER: US
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CLASSIFICATION:
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                                   TGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGG
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                                                                                                                                                                                                                                                     Length 3855;
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polypeptide"
1300 C; 1226 G; 678 T; 0 OTHER.
                                                                                                                                                                                                                                                     22;
                                              REFERENCE/DOCKET NUMBER: 015389-002600US TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    Score 1909; DB 22;
Pred. No. 0.00e+00;
                                                                                                                                                                                     variant polypeptide"
                                                                                                                                                                                                                                                                      0; Mismatches
08/724,643
                                         36,429
APPLICATION NUMBER: US 00
FILING DATE: 01-OCT-1996
              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T
REGISTRATION NUMBER: 36,
                                                                                                 LENGTH: 3855 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                    Query Match

Best Local Similarity 100.0%;
Matches 1909; Conservative
                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                          LOCATION: 56..2479
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                     SEQUENCE 3855 BP; 651 A;
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OTHER INFORMATION:
                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                  NAME/KEY: -
LOCATION: 1..3855
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NAME/KEY: CDS
      FILING DATE:
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                                    TCAGGCCCGGCCCCCGCCACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC
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Matches 1909; Conservative
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CAAGTICCIGCACIGCCIGAIGAGIGIGIACGICGICGAGCIGCICAGGICITICTITIA 1740
          TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAG
                                                                                                                                                                                                 Sequence 18, Application US/08911312
SECHARY CANT. CAND APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase.
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/911,312 FILING DATE: 14-AUG-1997 CLASSIFICATION: 536 CLASSIFICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
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US-08-911-312-18 STANDARD; DNA; UNC; 3855
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PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATE: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Einhorn, Gregory P. REGISTRATION NUMBER: 38,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 09-MAY-1 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-AUG-
                                                                                                                                                                                                                                                                                                                                                                     USA
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Pred. No. 0.00e+00;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 56..2476
OTHER INFORMATION: /product= "hTRT"
OTHER INFORMATION: /note= "clone #712562"
SEQUENCE 3855 BP; 651 A; 1300 C; 1226 G; 678 T; 0 OTHER.
REFERENCE/DOCKET NUMBER: 015389-002500US
        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 3855 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
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US-08-912-951-1 STANDARD; DNA; UNC;
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STRANDEDNESS: single
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DIAGNOSTIC AND
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Sequence 1, Application US/08912951

Sequence 1, Application US/08912951

CENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Chapman, Karen B.

APPLICANT: Maranura, Karen B.

APPLICANT: Andrews, William H.

TITLE OF INVENTION: HERAPEUTIC METHODS

CONTRESPONDENCE ADDRESS:

CONTRES
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: 435
ATONEN'AGENT INFORMATION:
NAME: APPLE, RANDOLPH T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/854,050
ELLING DATE: 09-MAY-1997
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION UNBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: APPR-1997
CLASSIFICATION: 435
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FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
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CACAGACCCCGGTCGCCTGGTGCAGCTGCTCCGCCAGCACACAGCAGCCTGGCAGGTGTA
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Pred. No. 0.00e+00;
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1363 C; 12
                                                            Query Match 99.4%;
Best Local Similarity 100.0%;
Matches 1909; Conservative
                                      OTHER INFORMATION:
SEQUENCE 4015 BP; 663 A;
       LOCATION: 56..3454
OTHER INFORMATION:
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                                                                                                              NAME/KEY: CDS
LOCATION: 56.3454
COTHER INFORMATION: /product= "human telomerase reverse
OTHER INFORMATION: transcriptase (hTRT)"
SEQUENCE 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 OTHER.
                                                                                                                                                                                                                                     Length 4015;
                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                             Score 1909; DB 24;
Pred. No. 0.00e+00;
0; Mismatches 0;
 4015 base pairs
                                                                                                                                                                                                                               query Match
Best Local Similarity 100.0%;
Matches 1909; Conservative
                   TYPE: nucleic acid STRANDEDNESS: single
                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                   FEATURE
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                               APPLICANT: Cach, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Maren B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and
TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,919
FILING DATE: 31-MAR-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 42,058
REBERBENG-ZPOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: WO PCT/US97/17885 FILING DATE: 01-OCT-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION 1973

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996

PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997

PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997

PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997

PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997

PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997

PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
1, Application US/09052919
                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Parent, Annette S
REGISTRATION NUMBER: 42,
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94111-3834
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191

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US-08-854-050-224 STANDARD; DNA; UNC;
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                GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA
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                                                                CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGCGACAAGGAGCAGCTGCG
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/note= "human telomerase reverse transcriptase (hTRT) catalytic protein Length 4015; NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "htrr"
OTHER INFORMATION: /note= "human telomerase revers
OTHER INFORMATION: transcriptase (htrr) catalytic
OTHER INFORMATION: component"
SEQUENCE 4015 BP: 663 A; 1363 C; 1275 G; 714 T; 0 OTHER. APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Novel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536 NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs Score 1909; DB 21; Pred. No. 0.00e+00; 0; Mismatches 0; CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 08/724,643
FILING DATE: 01-0CT-1996 STREET: Two bunce.
CITY: San Francisco
STATE: California PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MX-1997
CLASSIFICATION: 536 Application US/08854050 Application US/08854050 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: Query Match Best Local Similarity 100.0%; Matches 1909; Conservative nucleic acid Judence 224, Applicati Sequence 224, Applicati GENERAL INFORMATION: APPLICANT: Cech, The APPLICANT: List MOLECULE TYPE: CDNA linear STRANDEDNESS: TOPOLOGY:

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· 4	GCCGCTGGCCACGTTCGTGCGCGCCTTGGGGCCCCAAGGGCTTAGCTGCAGCGG	qΩ	12(
ò	GCCGCTGGCCACGTTCGTGCGCGCCTGGGGCCCCAGGGCTGCGGCGGCGGGGGGGG	Qy	12:
7 6	1 CANCACACAMATACACACAMATACACACACACACACACACACA	ପୁ	13(
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· 6	ACGGCCGCCCCCCCCCTCTTTCCGCCAGGTGTCTTGCTTG	qq	133
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<u> </u>	GGC ICCCAGC IGCGCC IACCAGG IG IGCGGGCCGCCIGIACCAGC ICGGCGC GCCAC	qq	16
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ογ	852 ccgrccacccacccacccrccrcrcrcrcrccrcccccccc	A C	×
qa a	901 CACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCA	: B U E	N N
3 6	941 CTPCTACCACCACCACCACCACCACCACCACCACCACCACCAC	388	į.
οy	972 GCACCACGGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC 103	888	
g :	1021 CCCGGTGTACGCCGAGACCAAGGACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCAGCTGCG 1080	8888	
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GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGCTGCGCAGGCTGCGCTGCGCAGGCTGCGCAGGCTGCGCAGGACTGCGCAGGACTGCGGACTGCGCACTGCGCAGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGA
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                                            GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCT
                                                                                                                                   GTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Hamilton, Brook, Smith & Reynolds, STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
S-09-026-981-35 STANDARD; DNA; UNC; 4023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 35, Application US/09026981
Sequence 35, Application US/09026981
GENERAL INFORMATION:
APPLICANT: Counter, Christopher M.
APPLICANT: Weinberg, Robert A.
TITLE OF INVENTION: Telomerase Catal
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
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                              COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1906; DB 23;
Pred. No. 0.00e+00;
0; Mismatches 2;
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REFERENCE/DOCKET NUMBER: WH197-11p4AM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEPHONE: 781-861-6240
                                                                                                                            PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/064,322
FILING DATE: 30-0CT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,762
FILING DATE: 14-A0G-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,549
FILING DATE: 01-AGG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/047,151
FILING DATE: 20-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/038,750
FILING DATE: 20-FEB-1997
ATTORNEY AGENT INFORMATION:
                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,981
FILING DATE: 20-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                           NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
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LENGTH: 4023 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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           1511 ACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCA 1570
                                                       1691 CCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGAGCTGCTCAGGTCTTTTTT 1750
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                                                                                       GGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGG 1682
                                                                                                                                 CCAAGITCCIGCACTGCTGATGAGTGTGTACGTCGAGCTGCTCAGGTCTTTTTT 1742
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                                            AGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGGCTGCGCT
                                                                                                                                                                                                                                                                  CALF: JALLA COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor STATE: California
COUNTRY: United States of America
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US-08-854-050-173 STANDARD; DNA; UNC; 4029 BP
                                                                                                                                                                                                                                                                                                                                                              Sequence 173, Application US/08854050
Sequence 173, Application US/08854050
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapmen, Karen B.
APPLICANT: Chapmen, Karen B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Novel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS: 225
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
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FILING DATE: 25-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 83.1%; Score 1596; DB 21; Length 40 Best Local Similarity 95.7%; Pred. No. 0.00e+00; Matches 1828; Conservative 0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..4029
OTHER INFORMATION: /note= "preliminary sequence for OTHER INFORMATION: human TRT cDNA insert of OTHER INFORMATION: plasmid pGRN121"
SEQUENCE 4029 BP; 687 A; 1342 C; 1255 G; 720 T; 25 OTHER.
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, Randolph T.
REGISTRATION NUMBER: 05,429
REFERENCE/DOCKET NUMBER: 015389-0029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
SEQUENCE CHARACTERISTICS:
LEUGHT: 4029 base pairs
TYPE: nucleic acid
STRANDENESS: single
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1871 CGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGCCCCCCCTGCTGACG 1920
                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
CLASSIFICATION: 536
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                                                                                                                                                                                                                       APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Maranta, Gregg B.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Novel Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Cz
STREET: Two Embarcadero Center, 8th Fic
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                           US-08-851-843-173 STANDARD; DNA; UNC; 4029
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PRIOR APPLICATION DATA
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: NAME: APPLE RADGIPh T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-0029
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
                                                                                                                                                                                          Sequence 173, Application US/08851843
Sequence 173, Application US/08851843
GENERAL INFORMATION:
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LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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         for
                              OTHER
                                            Length
         sequence 1
rt of
                              25
                                                           75;
LOCATION: 1..4029
OTHER INFORMATION: /note= "preliminary seq
OTHER INFORMATION: human TRT CDNA insert o
OTHER INFORMATION: plasmid pGRN121"
SEQUENCE 4029 BP; 687 A; 1342 C; 1255 G; 720 T;
                                            Score 1596; DB 21;
Pred. No. 0.00e+00;
                                                           0; Mismatches
                                            83.1%;
95.7%;
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                                                  Similarity
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Matches 1828;
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Sequence 6, Application Sequence 6, Application GENERAL INFORMATION:

RESULT 12
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APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2257 GGCAGCGCTGCGTCCTGCTGCGACGTGGGAAGCCCTGGCCCCGGGCCACCCCCGCGATGC 2316
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Pred. No. 0.00e+00;
0; Mismatches 0; Indels 104;
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SEQUENCE 4200 BP; 525 A; 1187 C; 1138 G; 644 T; 706 OTHER.
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
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                                                                                                                                                                                           STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 015389-002600US TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
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APPLICATION NUMBER: US 08/851,843
FILING DAIE: 06-MAY-1997
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
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APPLICATION NUMBER: 0S 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: 435
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FILING DATE: 25-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                         United States of America
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TYPE: nucleic acid
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Matches 1630; Conservative
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APPLICATION NUMBER:
FILING DATE: 25-APF
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3457 CAGCICICIGAGGCCCAGCCIGACIGGCGCICGAGGCICGIGGAGCCCAICIIICIGG 3516
                                                                                       1167 TICCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCGCCTACTG 1226
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APPLICANT: Allsopp, Richard
APPLICANT: DePinho, Ronald
APPLICANT: Greenberg, Roger
ADDRESSE: 101
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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US-09-042-460-1 STANDARD; DNA; UNC; 3496
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FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
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Pred. No. 0.00e+00;
0; Mismatches 592; Indels 84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "mouse telomerase reverse
trascriptase (mTRT) cDNA clone"
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transcriptase (mTRT) cDNA"
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TELECOMONUSCATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEGUENCE CHARACTERISTICS:
LENGTH: 3496 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRILING DATE: 01-0CT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17885
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/979,742
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/912,951 FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503 FILING DATE: 114-AUG-1997
UMBER: US 08/846,017
25-APR-1997
                                                                                                                                                                                                                 US 08/911,312
                                                                       US 08/851,843
                                                                                                                                               US 08/854,050
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APPLICATION NUMBER: US 08/FFILIG DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
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                                FILING LOLL DE PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 06-MAY-1997
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LOCATION: 10.3435
OTHER INFORMATION: /not
OTHER INFORMATION: trar
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23.6%;
Best Local Similarity 64.3%;
Matches 1216; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 1.3496
OTHER INFORMATION:
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                                               GAGCGGACGCCCCTTGGCCAGGGGTCCTGGGCCCACCGGGCAGGACGCGTGGACCGAG
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                         ATCCCTGAAAGAGCTGGTGGCCAGGGTTGTGCAGAGACTCTGCGAGGCGCAACGAGAAA
                                                                                                                CGTGCTGCTTTTGGCTTTGACTGCTTAACGAGGCCCAGGCGGGCCTCCCATGGCCTT
                                                                                                                                TGCATGGATGCTACTGTTGAGCCGAGTGGGCGACGACCTGCTGGTGCTGCTGCTGGCACA
                                                                                                                                                                                                                 CTGTGCTCTTTATCTTCTGGGGCCCCCCAGCTGTGCCTACCAGGTGTGGGGTCTCCCCCT
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                                                                                                                                                CACTAGTAGCGTGCGTAGCTACTTGCCCAACACTGTTATTGAGACCCTGCGTGTCAGTGG
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               CAGGCGGCTTGTGCAACCCGGGGACCCGAAGATCTACCGCACTTTGGTTGCCCAATGCCT
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CTGGCAGATGCGGCCCCTGTTCCAACAGCTGCTGGTGAACCATGCAGAGTGCCAATATGT~1270
                     GGACCGTGTCCCCGCTGCAGAGCACCGTCTGAGGGAGAGGATCCTGGCTACGTTCCTGTT
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                                                                                    CAGACTCCTCAGGTCACATTGCAGGTTTCGAACAGCAAACCAACAGGTGACAGATGCCTT
                                                                                                                                                                             ------GAACAGCCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Counter, Christopher M.
APPLICANT: Meyerson, Matthew
APPLICANT: Weinberg, Robert A.
TITLE OF INVENTION: Telomerase Catalytic Subunit Gene
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Hamilton, Brook, Smith & Reynolds, STREET: Two Militia Drive CITY: Lexington STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВР
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US-09-026-981-36 STANDARD; DNA; UNC; 3346
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36, Application US/09026981 Sequence 36, Application US/09026981 GENERAL INFORMATION:
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1782 GCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCA 1841
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Pred. No. 6.37e-213;
0; Mismatches 0; Indels
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 170
CARRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
SEQUENCE 535 BP; 105 A; 152 C; 173 G; 105 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 52: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     CARGEL AFFILATION NUMBER: US/08/911,312
FILING DATE: 14-AuG-1997
CLESSPITCATION S16
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: US 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: single
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Local Similarity 100.0%;
nes 259; Conservative
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Pred. No. 2.85e-234;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
SEQUENCE 3346 BP; 617 A; 1027 C; 965 G; 735 T; 2 OTHER.
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1211 AGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACG 1251
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                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH197-11p4AM
                                                                                      PRIOR APPLICATION: 432
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/064,322
FILING DATE: 30-0CT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,762
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/054,549
FILING DATE: 01-AUG-1997
PRIOR APPLICATION NUMBER: US 60/047,151
FILING DATE: 20-MAY-1997
PRIOR APPLICATION NUMBER: US 60/038,750
FILING DATE: 20-MAY-1997
ATTORNEY APPLICATION NUMBER: US 60/038,750
FILING DATE: 20-PEB-1997
ATTORNEY APPLICATION NUMBER: US 60/038,750
FILING DATE: 10F0PARTION:
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US-08-911-312-52 STANDARD; DNA; UNC; 535
                                   UMBER: US/09/026,981
20-FEB-1998
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Sequence 52, Application US/08911312
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS: LENGTH: 3346 base pairs TYPE: nucleic acid STRANDEDNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 14.6%;
Local Similarity 100.0%;
nes 281; Conservative
                                                                                CLASSIFICATION:
                                                         FILING DATE:
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Search completed: Thu Dec 24 16:09:24 1998 Job time: 3547 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

 $\ensuremath{\text{n.a.}}$  -  $\ensuremath{\text{n.a.}}$  database search, using Smith-Waterman algorithm with gap extension penalties as well as gap opening penalties MPsrch_nna

Thu Dec 24 15:07:06 1998; MasPar time 156.09 Seconds 573.790 Million cell updates/sec Tabular output not generated. Run on:

>US-08-951-733-13 (1-1920) from US08951733.seq (1 of 2) 1920 Description: Perfect Score: N.A. Sequence:

1 CACGCGTCCGGGCAGCGCTG.......CCAGGCCCGCCCTGCTGAGG 1920 GTGCGCAGGCCCGTCGCGAC......GGTCCGGGCGGGACGACTGC

TABLE default Gap open 30; Gap extend 1 Scoring table:

Dbase 0; Query 0 STD Nmatch

88822 segs, 23323279 bases x 2 Post-processing: Searched:

n-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1 Minimum Match 0% Listing first 45 summaries Database:

Mean 8.977; Variance 5.692; scale 1.577 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

iption Pred. No.
Description
B ID
Query Match Length DB
Query Score Match
Result No. Sco

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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Patent	Patent	Sequence	Sequence	Patent	Patent	Patent	Sequence	Patent	Patent
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8-2	US9	US9	us9	089	8-4	us9	8-4	8-4	8-4	8-1	8-2	us9	8-3	7-8	8-2	796	840	7-8	8-2	796	840	037	7-8	037	037
JS-08-273	Ę.	PCT-US95-0	PCT-US93-	PCT-US95-	JS-08-471	PCT-US95-	<b>US-08-471</b>	US-08-471	JS-08-471	JS-08-133	US-08-209	PCT-US94-0	US-08-300	JS-07-807	JS-08-299	5480796-8	5171840-8	JS-07-807	JS-08-299	5480796-1	5171840-	5457037-2	JS-07-872	5457037	545703
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242	1004	1386	611	59	65	99	99	9	69	84	84	84	84	225	225	1404	1404	640	1640	2061	2061	2253	2454	2625	336
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## ALIGNMENTS

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ADDRESEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
STATE: Alexandria
STATE: 1800 Diagonal Road, Suite 500
STATE: Alexandria
STATE: 0.5A
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Elloppy disk
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATE: PATENTIN DATE:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                             APPLICALL...
FILING DATE:
APPLICATION NUMBER: EP 91 114 30000
FILING DATE: 26-ANG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMUTUNICATION INFORMATION:
TELEPHONE: (703)836-9300
mTTELEPHONE: (703)683-4109
                                                                                                APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
          US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
                                            Sequence 14, Application US/08232463 Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
RESULT
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ZIP: 94105-1493
COMPUTER READABLE FORM:
                                                                                                                                              TOPOLOGY: line IMMEDIATE SOURCE:
                                                                                                                                    STRANDEDNESS:
 FILING DATE:
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                                   NAME:
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                                                                                                                                                                                                   1101 CCTACTCAGCTCTCTGAGGCCCAGCCTGGCGCTCGGAGGCTCGTGGAGACCATCTT 1160
                                                                                                                   1161 TCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGGCCTGCCCCAGCG 1220
                                                                                                                                                                                                                                                                                                  1221 CTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTA 1280
                                                                                                                               Gaps
                                                                                                  ;
0
                                                    CLONE: pT2gpt-F1s
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                              3.5%; Score 67; DB 1; Length 7218; 2.4%; Pred. No. 1.19e-24; rvative 211; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VI
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                 T. 2
US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DX
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                1281 CGGGGTGCTCCTC 1293
                                                                                                                                                                                                                                                                                                                                     1415 YYYYYYYYYYY 1427
                                   linear
                                    TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                   XXXXXX
                                                                                                    Matches
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Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: BARAYITT, Alan
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEANUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1850 CTCTTCAAGTGCTGTCTGAATTCCAATGCTTTGCAACTTGCTCCAGACACTCTCCGGTAG 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1730 TCGACGACGTACACACTCATCAGCCAGGGAACTTGGCCAGGATCTCCTCACGCAGA 1671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1670 CGGTGCTCTGGGGCGGGAACACACACACACGGCTCCTGGGCTCCTGGCAAGCGCAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1610 GCCACGCTCATCTTCCACGTCAGCTCGCAGCGAGCTTGGCATGCTTCCCC 1557
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SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.3%; Score 44; DB 1; Length 7218 Best Local Similarity 0.8%; Pred. No. 2.87e-11; Matches 3; Conservative 196; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                      REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-238-163-5 STANDARD; DNA; UNC; 215 BP
EP 91 114 300.6
                                                                                   29,768
                                                                                                                                                                              TELETA 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                           14:
                  FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                              NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                      single
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 YNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 AMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 MSSSSVVSRTASCUDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSAN 65
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Sequence 100, Application PC/TUS9511934

GENERAL INFORMATION:

APPLICANT: Cytogen Corporation

TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From

TITLE OF INVENTION: Peptide Libraries

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds

STREE: 1155 Avenue of the Americas

CITY: New York

COUNTY: New York

COUNTY: USA

COUNTY: USA

COMPUTER READABLE FORM:

MEDIDIM TIPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 1; Length 215;
Pred. No. 2.19e-06;
76; Mismatches 95; Indels
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                          CURKENI AFFLLCATION DAIA:

PEPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 80
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Revin L.
REGISTATION NUMBER: 34,774
REFERNCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEFEX: (415) 543-9600
TELEFX: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T. 5
PCT-US95-11934-100 STANDARD; DNA; UNC; 74
                                                                                                                                                                                                                                         2307E-540
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FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.8%;
Best Local Similarity 13.2%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1435 TGCTGTGCTGGCGGAGC 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 KSNVSNNCGGGNKRDVS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BONNET, Alan
APPLICANT: POMELL, Ann
APPLICANT: PART INHIBITORS OF FUNGAL
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 HTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTAMTSRNRTGKTANNAVD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| ::| ::: : :: : :: | :| :| :| :| :| :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 SRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGTKSNVSNNCGGGNKRDVS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: Standard_name= "Deduced amino acid
OTHER INFORMATION: Sequence of PGIP from bean."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California CONNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.8%; Score 34; DB 1; Length 215; Best Local Similarity 12.9%; Pred. No. 7.29e-06; Matches 17; Conservative 56; Mismatches 59: TnAble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: sequence of PGIP from bean." SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                     APPLICATION NUMBER: US/08/238,163
CLASSIFICATION NUMBER: US/08/238,163
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Revin L.
REGISTRATION NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQUENCE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .r 4
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 SYANNKCCGSSC 214
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250 GCACGGCCGCC 261
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PCT-US95-11934-98 STANDARD; DNA; UNC; 81 BP.
             Query Match 1.4%;
Best Local Similarity 11.4%;
Matches 8; Conservative
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Best Local Similarity 11.4%;
Matches 8; Conservative
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480 CCCCACGCC 471
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                                                                                                     63 BNNBNACGCC 72
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ID PC
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Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                       Query Match 1.4%; Score 26; DB 2; Length 74; Best Local Similarity 10.3%; Pred. No. 7.10e-02; Matches 7; Conservative 20; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDICAL TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFRENGE/SDOCKET NUMBER: 1101-196-228
RECECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELER: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDRESS: single
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 118 872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 100: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                                                   T 6
PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                 481 GCCCCCAC 474
                                                                                                                                                                                                                                                                             63 VNNACCAC 70
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                                                                                                                                                      540 GAGCGCGCAGCGTGCCAGCAGGTGAACCAGCACGTCGTCGCCCCACGCGGCGCAGCAGCAG 481
                                                                                                    APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Applide Libraries
TITLE OF INVENTION: Peptide Libraries
CORRESPONDENCE: 103
ADDRESSE: ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
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Score 26; DB 2; Length 74;
Pred. No. 7.10e-02;
19; Mismatches 43; Indels
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Pred. No. 7.10e-02;
19; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.
                                                                                                                                                                                                                                                                                                                                  T 7
PCT-US95-11934-92 STANDARD; DNA; UNC; 81 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95/11934 FILLING DATE: 20-SEP-1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 92, Application PC/TUS9511934 Sequence 92, Application PC/TUS9511934 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-:
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 790-9090
TELEFAN: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDENESS: single
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158 regegecechagegeregesegeregagegegegegegegegegegereg 217
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Sequence 97, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.4%; Score 26; DB 2; Length 82; Best Local Similarity 15.2%; Pred. No. 7.10e-02; Matches 12; Conservative 20; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: NEW JOIN
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLING DATE: 20-SEP-1995
                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFEX: (614) PENNIE
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 82 BP; 1 A; 2 C; 10 G; 8 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JT 10
PCT-US95-11934-97 STANDARD; DNA; UNC; 82 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leaslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
RELECOMMUNICATION INFORMATION:
TELECHONE: (212) 790-9090
TELEFRAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 82 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 NNBNNBNNBGGTTGTG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XXXXXX
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C Sequence 97, Application PC/TUS9511934
C GENERAL INFORMATION:
C APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Peptide Libraries
C TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES:
C CORRESPONDENCE ADDRESS:
C ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
C CITY: New York
C CITY: New York
C CONTRY: USA
C ZIP: 10036
                                  Sequence 98, Application PC/TUS9511934
Sequence 98, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 1.4%; Score 26; DB 2; Length 81; Best Local Similarity 14.3%; Pred. No. 7.10e-02; Matches 10; Conservative 19; Mismatches 41; Indels
                                                                                                                                                                                                                                                   STATE: New YORK
COUNTRY: USA
21P: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
NAME: MISTOCK, S. LEGALE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEPRATION NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEPRATION NUMBER: 1101-196-228
TELEPRATION NUMBER: 1101-196-228
TELEPRATION NUMBER: 1101-196-228
TELEPRATION NUMBER: 1000-099:
TELEPRATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENTH: 81 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
SEQUENCE 81 BP; 6 A; 6 C; 4 G; 5 T; 60 OTHER.
                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                л 9
PCT-US95-11934-97 STANDARD; DNA; UNC; 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                     STREET: 1155 Ave
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1455 GCCGTACACC 1446
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                                                                                                                                                                                                                                                                                     APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                    ADD...
STREE. 1155...
CITY: New YORK
CITY: New YORK
STATE: New YORK
COUNTRY: U.S.A.
IP: 10036-7711
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,052A
FILING DATE: 06-JUNE-1995
FILING DATE: 06-JUNE-1995
                                                                                          Score 26; DB 2; Length 82;
Pred. No. 7.10e-02;
20; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 1; Length 66;
Pred. No. 2.09e-01;
18; Mismatches 37; Indels
                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 82 BP; 1 A; 2 C; 10 G; 8 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA
SEQUENCE 66 BP; 2 A; 3 C; 4 G; 2 T; 55 OTHER.
                                                                                                                                                                                                                .T 11
US-08-471-052A-144 STANDARD; DNA; UNC; 66 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
ATORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-179
TELECOMMUNICATION INFORMATION:
TELEFPHONE: 212 790-9090
TELETAX: 6644 PENNIE
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                   Sequence 144, Application US/08471052A Sequence 144, Application US/08471052A Patent No. 5625033 GENERAL INFORMATION:
TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                             LENGTH: 82 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                           Query Match
Best Local Similarity 13.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 11.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                    265 CGGGGGGGGCGTG 251
                                                                                                                                                                   66 NBNNBNNBGGTTGTG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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GENERAL INCRMATION:
APPLICANT: PLOCKOP, Darwin J.
APPLICANT: Ala-Kokko, Leena
APPLICANT: Ala-Kokko, Leena
APPLICANT: Ritvaniemi, Pertti
APPLICANT: Ritvaniemi, Pertti
APPLICANT: Baldwin, Clinton
APPLICANT: Applicant: Almad, Nilofer Nina
TILLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988ris
STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 GCCCGCCGCCCGCCCGCCGCCGCCGCCAGGAGCCCTTCAAGG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 1; Length 68;
Pred. No. 2.09e-01;
0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
SEQUENCE 68 BP; 7 A; 38 C; 17 G; 6 T; 0 OTHER.
л. 12
US-07-977-284A-243 STANDARD; DNA; UNC; 68 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,284A
FILING DATE: 13-NOV-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 13
US-08-471-052A-142 STANDARD; DNA; UNC; 69
XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0697
TELECOMMUNICATION INFORMATION:
TELEFAN: (215) 568-3100
TELEFAN: (215) 568-3439
INFORMATION FOR SEQ ID NO: 243:
SEQUENCE CHARACTERISTICS:
                                                                                   Sequence 243, Application US/07977284A Sequence 243, Application US/07977284A Patent No. 5558988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.3%;
Best Local Similarity 75.5%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 68
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: LINEAR
TI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: PA
COUNTRY: US
ZIP: 19103
                                          XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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Sequence 100, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: CYTOGON COMPORATION
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25; DB 2; Length 74;
Pred. No. 2.09e-01;
20; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIREE:: 125 AVENUE OF THE AMERICAS
CITY: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEB PC COMPATIBLE
COPPUTER: TEB PC COMPATIBLE
COPPUTER: PATENTIN PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATORNEY/AGENT INFORMATION:
NAME: MISTOCK: S. LESIIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 1101-196-228
REGISTRATION NUMBER: 1101-196-228
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: (A12) 869-9741/8864
TELEFAX: A base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TOPOLOGY: linear
MOLECULGY: DNA (genomic)
SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
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PCT-US95-11934-100 STANDARD; DNA; UNC; 74 BP.
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Best Local Similarity 8.7%;
Matches 6; Conservative
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                   Sequence 142, Application US/08471052A
SETEMENT: REAV. B. K.
APPLICANT: FOWLKES, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COUNTRY: U.S. A.
STREET: 1155 Avenue of the Americas
STREET: 1155 Avenue of the Americas
COUNTRY: U.S. A.
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COUNTRY: U.S. A.
COUNTRY: U.S. A.
COMPUTER: TOPPY disk
TELEPHONE: TOPPY disk
TELEPHONE
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Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25; DB 1; Length 69;
Pred. No. 2.09e-01;
18; Mismatches 37; Indels
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SEQUENCE 69 BP; 2 A; 4 C; 6 G; 2 T; 55 OTHER.
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PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
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Best Local Similarity 11.3%;
Matches 7; Conservative
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STATE: New York
COUNTRY: USA
ZIP: 10036
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Search completed: Thu Dec 24 15:09:57 1998 Job time: 171 secs.

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release 3.1A John F. Collins, Blocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd		
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Run on: Thu Dec 24 16:09:43 1998; MasPar time 2754.39 Seconds	33 0	
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Title: >US-08-951-733-13 Description: (1920-2820) from US08951733.seq (2 of 2) Parfert Sonre: 901	9 7 8 6 9 8 7 8	5333
N.A. Sequence: 1920 GTCCAGACTCCGCTTCATCCAGGCCCTGGGTGGCACGGCT 2820 Comp:	0 4 4 0 4 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1	
Scoring table: TABLE default Gap open 30; Gap extend 1		
Nmatch STD : Dbase 0; Query 0	45	
Searched: 567134 seqs, 1101898692 bases x 2		
Post-processing: Minimum Match 0% Listing first 45 summaries	RESULT	H
Database: emb155	DEFINITION	HOMO Say
	ACCESSION NID KEYWORDS	
Database: genbank107 15:9b_ba1 16:9b_ba2 17:9b_htg 18:9b_in 19:9b_om 20:9b_ov 21:9b_pat 22:9b_ph 23:9b_pl1 24:9b_pl2 25:9b_pr1 26:9b_pr2 27:9b_pr3 28:9b_ro 29:9b_st 30:9b_sts 31:9b_sy 32:9b_un 33:9b_un 33:9b_v	SOURCE ORGANISM	human. Homo sag Eukaryol Vertebra
Statistics: Mean 10.599; Variance 5.047; scale 2.100	REFERENCE AUTHORS	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	TITLE JOURNAL MEDLINE	And Tel Sci 974
SUMMARIES	REFERENCE	
Result Ouery No. Score Match Length DB ID Description Pred. No.	TITLE JOURNAL	Direct Submitte
4015 27 AF015950 Homo sapiens telomeras 4027 27 AF018167 Homo sapiens telomeras 8960 31 AF043739 Synthetic construct hu	FEATURES SOURCE	ø
369 41.0 3369 28 AF073311 369 41.0 3426 28 AF051911 39 4.3 7218 21 166494		
34 3.8 74371 26 AC005369 Homo sapiens chromosom 30 3.3 2152 128878 Sequence 5 from patent	dene	
29 3.2 15807 15 28 3.1 215 21 26 3.1 215 21	CDS	
20 Z.9 3591 13 AFUZ/499 AZOTODACTEF VINELANDII		

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rect Submission
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llo Park, CA 94025, USA
llo cation/Qualifiers
1. 4015
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/ 11 4015
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ura, Catarrinii; Hominidae;

ura, T.M., Morin, G.B., Chapman, K.B., Weinrich, S.L.,

ws, W.H., Lingner, J., Harley, C.B. and Cech, T.R.

arase catalytic subunit homologs from fission yeast and human;

277 (5328), 955-959 (1997)
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rata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Rattus rattus protein 3CH134/CL100 Prpase=ox. R. norvegicus mRNA for Sequence 14 from paten H.sapiens mRNA for Uli R. norvegicus HISHR mRN eryk-malonyl-coenzyme Saccharopolyspora eryt Homo sapiens mRNA for Volvox carteri acetola Rat calcium channel al Rattus norvegicus pore Human cosmid UlCA16, c Amycolatopsis mediterr *** SEQUENCING IN PROG Rhodobacter capsulatus fomo sapiens Chromosom *** SEQUENCING IN PROG Rhodobacter capsulatus fomo sapiens Chromosom *** SEQUENCING IN PROG Sequence 142 from paten Sequence 142 from paten Sequence 120 from paten Mouse histidase locus Pseudomonas aeruginosa Bombyx mori LIBm DNA, Hepatitis E virus ORPI Hepatitis E virus Com C. elegans cosmid K12H Amycolatopsis mediterr Amycolatopsis mediterran Amycolatopsis me
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/product="telomerase reverse transcriptase"
/db_xref="PID:92330017"
/translation="MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDP
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0; Mismatches 0; Indels
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/COGULS_ALL_1
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Meyerson,M., Counter,C.M., Eaton,E.N., Ellisen,L.W., Steiner,P.,
Caddle,S.D., Ziaugra,L., Beijersbergen,R.L., Davidoff,M.J., Liu,Q.,
Bacchetti,S., Haber,D.A. and Weinberg,R.A.
Direct Submission
Submitted (11-Aug-1997) Whitehead Institute for Biomedical
Research, Massachusetts Institute of Technology, Nine Cambridge
Center, Cambridge, MA 02142, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meyerson, M., Counter, C.M., Eaton, E.N., Ellisen, L.W., Steiner, P., Caddle, S.D., Ziaugra, L., Beijersbergen, R.L., Davidoff, M.J., Liu, Q. Baccheti, S., Haber, D.A., and Weinberg, R.A.
hEST2, the putative human telomerase catalytic subunit gene, is purequiated in tumor cells and during immortalization cell 90 (4), 785-795 (1997)
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Homo sapiens telomerase catalytic subunit (hEST2) mRNA, complete
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/gene="hEST2"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/map="5p15.33"
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LDDIHRAWRTFVLRVRAODPPELTSYKVALFSVLAYERARRPGLLGASVLG

LDDIHRAWRTFVLRVAODPPELTSYKVANTGAYDTIFODRILTEVIASIIKRONTY

VRRYAVVOKAAAHGHVRKAFKSHVSTLDDLQPYNRQFVAHLOFTSFLRDAVVIEOSSST

IRASSGLEDVELKRWGHHAVBIRGKSYVQCGIPOGSILSTLLCSLCSGDBENKLFAG

GGTARVOMPHGHGLFPWGGLLLDTRILERVGSDSSSSAMTSIRASLTFNRGFKAGNNMR

KLFGYLRKGHSLFLDLQVNSLATOTNIKKILLLQAYRFHACVLQLPFHQQVWKNPT

FFLRYISDRASLCSILKAKNAGMSLGARGAAGPLPSBAVQMLCHQAFLLKITRHRYT

FYPLLGSLRPAQTGLSKLLPTTLALLEAAANPALPSDFKTILD"

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Best Local Similarity 100.0%;
Matches 901; Conservative
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/product="telomerase catalytic subunit"
/db_xref="plD:g3023055"
/db_xref="plD:
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LLROHSSPWOVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQEL
TWRMSVRGCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTET
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SPROGLRPFYRMDYVVGARTFRREKRAERLTSRYKALESVLXYERARRFOLLGASVLG
LDDIHRARRTFYRAQDPPPELYFVKVNTGAYDTIPODRLTEVIASIIKPONTYC
VRRXAVVQRAAHGHVRKAFKSHVSTLTDLOPYMRORYAHLOGTSPLRDAVVIROSSSL
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IRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEAL
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order(1. 1101,4606. 8960)
/note="mammalian expression vector; see GenBank Accession
Number 047120"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic construct human telomerase catalytic subunit (hTERI/hESI2) mRNA and 3' Influenza A hemagglutinin tag, complete
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Submitted (20-JAN-1998) Whitehead Institute, 9 Cambridge Center,
Cambridge, MA 02142, USA
Location/Qualifiers
1. 8960
/organism-"synthetic construct"
GAACTIGCGGAAGACAGIGGIGAACTICCCIGIAGAAGACGAGGCCCIGGGIGGCACGGC_2809
                                     /organism="Cloning vector pCI-neo"
/db_xref='taxon:45772"
1102. .4542
/note="telomerase catalytic subunit hTERT/hEST2
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1208e="hTRET/hEST2"
1147. .4605
/note="telomerase/reverse transcriptase"
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/db_xref="taxon:9606"
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1 (bases 1 to 8960)

Counter, C.M., Meyerson, M., Ea
Haber, D.A. and Weinberg, R.A.
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KEFOYLRKOHSLFLDLQVNSLQTYCTNIYKILLDQAYRFHACVLQLPFHQOWRNPT
FFIRST SILKAKURAGMSLGARGAAGPLLPSAVQWLCHQAFLLKLTRHRVT
YVPLLGSLRTAQTQLSRKLPGTTLTALBAAANPALPSDFKTILDYPPTAGYPYD
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/note="engineered based on the epitope for the anti-influenza virus hemagglutinin monoclonal antibody 12C45; similar to part of the Influenza A hemaglutinin gene sequence in GenBank Accession Number M29257"
/db_xref="taxon:32630"
a 2551 c 2484 g 2038 t 1 others
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Pred. No. 0.00e+00;
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Martin-Rivera, L., Herrera, E. and Blasco, M.A.

Direct Submission
Submitted (19-JUW-1998) Immunology and Oncology, National Centre of Biotechnology, Cantoblanco, Madrid 28049, Spain
Location, Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRFVDDFLLVTPHLDQAKTFLSTLVHGVPEYGCMINLQRTVVNFPVEPGTLGGAAPYQ
LPHCLFPWGCLLLDYQTLEYFCDYSGXAQYSIKTSLTFGSVFRAGKTMRNKLLSVLR
LKCHGLFLDLQVNSLQTVCTNIYKFELLQAYRFHACYQLPFDQRVRKNLTFFLGIIS
SQASCCYALLKVKNDGMTLRASGSFPPEAAHNLCYQAFLLKLAAHSVIYKCLLGPLRI
                                                                                                                                                                                                                                                                                                                       house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 3369)

Martin-Rivera,L., Herrera,E., Albar,J.P. and Blasco,M.A.

Expression of mouse telomerase catalytic subunit in embryos and adult tissues

Proc. Natl. Acad. Sci. U.S.A. 95 (18), 10471-10476 (1998)

98393668
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                                                                                                                                                                                                                              3369 bp mRNA ROD 09-SEP-1998 telomerase catalytic subunit mRNA, complete cds.
                                                       2760 GAACTIGCGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGC
2700 CCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGT
                                   3840 GAACTIGCGGAAGACAGTGGTGAACTICCCTGTAGAAGACGAGGCCCTGGGTGGCACGGC
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Pred. No. 7.56e-290;
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Greenberg, R.A., Allsopp, R.C., Chin, L., Morin, G.B. and DePinho, R.A. Expression of mouse telomerase reverse transcriptase during development, differentiation, and proliferation
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                                                                                                                      CATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCC---AGAACAC
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                     GACTCTTCAGCATGCTCAACTATGAGCGGACAAAACATCCTCACCTTATGGGGTCTTC
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LVPPSCAYQVCGSPLYQICATTDIWPSVSASYRPTRPVGRNFTNLFLQIKSSRQE
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Oncogene (1998) In press 2 (bases 1 to 3426) (bases 1 to 3426) (bases 2 to 3426) (bases 2 to 3426) (bases 2 to 3426) (bases 2 to 34180pp,R.C., Chin,L., Morin,G.B. and DePinho,R.A. Direct Submission Submitted (02-MAR-1998) Microbiology and Immunology, Albert Pinstein College of Medicine, 1300 Morris Park Ave., Bronx, NY
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                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .3426
/organism="Mus musculus"
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DNA PRI 01-AUG-1998
5, BAC clone 119j3 (LBNL H175), complete
2534 AGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGCTCCATCCTCCCACCGTGCTCCTGCA 2593
                                                           Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 74371)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M., Sequencing of human chromosome 5
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DOE Joint Genome Institute.

Location/Qualifiers
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Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.
Davis,C.A., Kadner,K., Miguel,T., Pitluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
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2 (bases 1 to 74371)
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onplement(7830, .8185)
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complement(join(38063. 38218,38462. 38578,38741. 38995,39071. 39205,39532. 39630,39935. 40048,40300. 40410,40503. 40661,41868. 41972,42103. 42225,42492. 42569, /rpt_unity="%n" / rpt_unity="%n" / rpt_unity="%n" / rpt_family="%nem20" / rpt_family="%nem20" / rpt_family="%nem20" / rpt_family="%nute="GRMiL 2 excellent exon, frame 0" / rpt_family="%nute" / rpt_family="%nute" / rpt_family="%nute" / rpt_family="%nute" / rpt_family="%nute" / rpt_family="%nute" / rstandard_name="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%norpt="%nor /standard_name="histidyl-tRNA synthetase" /note="78%-100% protein identity GenPept:U18937" complement(38069..38215) /note="GRAIL 2 excellent exon, frame 0" complement(38462..38578) complement(34021. .34144)
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32617. 33208
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complement(33509. 33785) complement(25349. .25713)
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complement(25727. .26471)
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Note: remainder of annotations omitted.

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7113. .7373
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Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete
                                                                          Db 15918 KCKCTSTSKCSCMSRSKSKRGWGYRSWKKYRCAMWITCKSSKCWCWSYRMRWKCYSCSYC 15977
                                                                                              1 (bases 1 to 215)
1 (bases 1 to 215)
2 (bases 1 to 215)
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to
control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 7431).
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
Sequencing of human chromosome 5
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Kimmerly, W. Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Davis,C.A., Kadner,K., Miguel,T., Pitluck,S., Pollard,M.,
Rojeski,H., Subramanian, S. and Martin,C.H.
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Pred. No. 1.16e-03;
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           Score 34; DB 26; Length 743
Pred. No. 3.54e-06;
46; Mismatches 25; Indels
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91819054
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8 c 25 g
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Best Local Similarity 14.8%;
Matches 16; Conservative
             Query Match 3.8%;
Best Local Similarity 15.5%;
                                             13; Conservative
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Unclassified.
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AUTHORS
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Direct Submission
Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A.
Sequence submitted by:
DOE Joint Genome Institute.

Location/Qualifiers
1. 74371
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'note="(A)29"
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MEU72662 15807 bp DNA BCT 06-JUN-1997

Methylobacterium extorquens methylotrophy region containing malyl-CoA lyase (mclA), putative ABC transporter subunit A (abcA), putative ABC transporter subunit (abcC), methanol dyhydrogenase large subunit (formoeopterin aldolase (folB) and dihyrdoxypteroate synthase (folC) genes, complete cds, and phosphoeolpyruvate carboxylate (ppcA) gene, partial cds, and pyrroloquinoline quinone biosynthesis gene cluster containing PqqE (pqqE) gene, complete cds, and PqqC/D gene, partial cds.
                                                                                                                                                                                    (bases 1 to 13697)
Chistoserdova, L. and Lidstrom, M.E.
Molecular and mutational analysis of a DNA region separating two methylotrophy gene clusters in Methylobacterium extorquens AM1
Microbiology 143 (Pt 5), 1729-1736 (1997)
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Pred. No. 1.16e-03;
63; Mismatches 53; Indels 0
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complement(33670. 33785)
/rpt_family="Alu"
complement(34021. 34144)
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Methylobacterium extorquens
                             /rpt_family="Alu" 32977. .33088
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Best Local Similarity 14.7%;
Matches 20; Conservative
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// (Tpt_family="Alu" | 1011(29485. 29598. 29779) | 1011(29485. 29596 | 29789) | 1011(29485. 29976 | 29495. 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 29976 | 2997
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9475. . 10065
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1887. .1861
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TARLGIIGFCWGGRITWLYAAHNPAVKAGVAWYGRLVGDSSALMPKNPVDVAADLKAP
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LFRDCRVFRLVLDEVEKTLLMVDLEIARDYAGLVEDAGIRARIFGMIEAEYTLTREMV
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GWKRLQDWFRQYGVA"
                                                                       Toyama, H., Chistoserdova, L.V. and Lidstrom, M.E. Sequence analysis of pqq genes of Methylobacterium extorquens AM1 required for biosynthesis of pyrroloquinoline quinones and purification of a biosynthetic intermediate
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1887. .2156
                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (26-SEP-1996) Chemical Engineering, University Washington, Box 351750, Seattle, WA 98195, USA
On Jun 6, 1997 this sequence version replaced g1:1408258
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Chistoserdova, L. V. and Lidstrom, M.E.
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1. .15807
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/gene="abcA"
/codon_start=1
/transl_table=11
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/transl_table=11
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/codon_start=1
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4284. .5279
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2506 ACATGAAGCGTAGGAAGACGTCGAAGAGGCCCACTGCTGGCCTCATTCAGGGAGGAGCTCT 2447
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120. .1571
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/gene="algG"
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pyrophosphokinase"
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complement(11823. .12618)
GNMPFSERKGGGFENKIAQIVADELKVKLRYYWLTQGPGFVRNTLGTGLCDLIIGTSG
GDIVQATUPYYSAAYTLVARKGELADIKRLDDPRLKDRQIGIIAGTPPSNKLSELKLV
GERTHAYAPYAFGAAERYYVAAEVIDLAEKKIDVAILMGPAAGWLAKQSGVPMDVV
PLLHEPGRAALTFRVSMGYRHRSDWRRSLINTVERKRADIEAYTREYSVPLLAEEDT
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Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A $ 29-OCT-1996;
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Pred. No. 1.85e-02;
62; Mismatches 84; Indels
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                                                                                                     /gene="folA"
complement(10966. .11442)
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/gene="folB"
                                                                                     complement(10966. .11442)
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Sequence 5 from patent US 5569830.
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                                                                                                                                      /gene-"folA'
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Best Local Similarity 67.9%;
Matches 55; Conservative
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/product="Algx"
/db_xref="PID:92920566"
/translation="MKTHNSKWIGPAALAAAIALAAAGVRAEETPTGLPVYRAESCCD
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FRSKGVELUTVYQPPRGWVQRNKLLPADYARPDYDKAYNNFRATLKHFEQLGYWYDDL
TPLIDEKVEPAFYFRGDHHWTSYGABSARIVKEIPAFADIPRKEFVTKKWGRM
GKRGTHHRVAGQLCNTTYAFBHSDQFFTEPRGEGGGDLGDSSLPQ1ILVGTSHSGTN
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DRYEYRQALSMGANGSEGKTLLAGKTYLLRGERGKEVLINGAGRLVEATNSRHQYDIR
FSDPSVKLEGTINYHGRRERFGPKPVTPETNGRFAFNMRDEADWGGLNFFAMEIQ
PPEGLKEPVEVEVRLCKRHDYHAPANLIARSGN"
                                                                                                                                                                                                                                                                                                      AF027499 5591 bp DNA BCT 01-MAR-1998
Azotobacter vinelandii mannuronan C-5-epimerase (algG) gene,
partial cds; and AlgX, alginate lyase (algL), AlgI, and AlgV genes,
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                                         95 IDSYNASGISSSNGGIDGNRSGADSYGSSKIAMISRNRIGKTANNAVDSRNMGDASVGSD 154
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1 (bases 1 to 5591)
Vazquez,R.A., Alvarado,D.A., Guzman,J., Soberon-Chavez,G. and
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1580. .2704
/gene="algt."
/note="Algt, similar to Pseudomonas aeruginosa Algt."
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Submitted (30-SEP-1997) Microbiologia Molecular, Inst. de
Biotecnologia. UNAM, Av. Universidad s/n Col. Chamilpa, Cu
Morelos 62210, Mexico
Location/Qualifiers
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/db_xref="PID:g2920565"
/translation="LEDKQEEILDLLVRRQKAVLIDPVVDPAQAEL"
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                                                                                                                                                           155 KNTKKHAKNSADGKVGSKNNGDRNNRYGTGTKSNVSNNCGGGNKRDVSSY 204
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    /organism="Azotobacter vinelandii"

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/transl_table=11
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Unpublished
2 (bases 1 to 1908)
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Local Similarity 71.2%;
hes 42; Conservative
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                                  Qian, Z.
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                                  AUTHORS
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AUTHORS
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REFERENCE
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AAFERHYADDEPEPIKKLGTNLWAALDTYLFGEGEGFGVVTGANOWLESDEEFKPAAS
ONTDWOALIOGVRETLARNNVOLVAAILPARARLYENFGEGOPASLHEDILYGNFRR
IVADAGIOAPDLLGFLOOARAGGOVFLRTDTHWTPYGAQVVAGOLATIKPIGVLFS
GNOYYTETLEFGGPHKGDLTHFLDLDPLEELLLPPPDQLARHYRQQESAFAGDDLFS
GNOYYTETLEFGSPAGGDDLFS
GNOYYTETLESGSPAGDDLFS
GNOYYTETLESGSPAGDDLFS
STOVPYALVGTSYSADERWNRAGALRQALGSDLVNRAEDGRGPLLPMLKFLOSEDFKK
SPPRLYIWEFPERYLPMAYDLSEFDADWIAQLKAAGRQDKQLADNTATNQGARH"
                                YMEKGRAGDLECTLAWLDAWAEDGALLTTEYNHTGKSMRKWALGSLAGAYLRLKFSSS
QPLAAYPEQARRIESNFAKVGDQVIKDWSDLPIKRINHSYWAAWAAWAAAGYATURRP
LEDWAVEQFHTAAGQVDSNGFLPHELKRRQRALAYHWSLPPLMMYAAFALANGVDLR
GDNDGALGRLAGVILAGVEKPEPFABRAGDEDODMEDLETDAKFSWLEPYCALYSGSP
ALRERKAEMGPFKNFRLGGDVTRIFDPAEKSPRSTVGKRD"
                                                                                                                                                                                                                                                                                                              FPHLIAGPVLRFRDLVDGFNHRTHTLDKFAEGCTRFWQGFIKKVFIADSLAPIADHCF
ALSPPTTGADAMLGALAYTAQLKPDFSGYSDMAGLGGLAUGFRFWHNFNDPYISOSITE
FWRRHISLGSFWLRDYLYISLGGRRGTTFQTYRNLILIMLLGGLWHGANWTFIIWGAM
HGTWLAIERALRIDAAPKTIRPLRWVFAFLLVMVGWVIFRAENLDVARWMYAAMFSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DWILSDLNKAQLISLQIATLLIAYVVIAVYGIRQFYAQPLIGAPKAKANDQADAPQGI
VHASSGTLAYSQAIDIPALATRVAVLLLFAASVLKLSAQSFSPFLYFQF"
V4409. .5575
4409. .5575
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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1 (bases 1 to 1905)
Qian, Z., Gilbert, M.E. and Kandel, E.R.
Differential induction by neuronal activity in rat brain of a protein tyrosine phosphatase containing a nuclear-localization signal
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                                                                                                                                                                                        2897. .4396
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2897. .4396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4409. .5575
/gene="algy"
/cote="similar to Pseudomonas aeruginosa Algy"
/codon_start=1
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Pred. No. 2.66e-01;
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larity 82.5%;
Conservative
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/product="protein tyrosine phosphatase"
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/tdb_yref="TD:9409023"
/tdb_y
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Submitted (15-OCT-1993) Zhuo Qian, Center For Neurobiology and Submitted (15-OCT-1993) Zhuo Qian, Center For Neurobiology and Behaviour, Howard Hughes Medical Institute, Columbia University, 722 West 168th Street, New York, NY 10032 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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phosphatase; This sequence comes from Fig. 1"
/codon_start=1
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Pred. No. 9.67e-01;
0; Mismatches 17; Indels
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115. .1218
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/db_xref="taxon:10118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="brain"
127. .1230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
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/Product="dual specificity phosphatase"
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CSSCSTPLYDQGGPVELLSFLYLGSAYHASRKDMLDALGITALINVSANCPNHFEGHY
OYKSIPVEDNHRADISSWFNBAIDFIDSIKDAGGRVEYHCQAGISRSATICLAYLMT
NRVKLDBAFFEVKQRRSIISPNFSFMGQLLQFESQVLAPHCSAEAGSPAMAVLDRGTS
TTTVFNFPVSIPVHPTNSALNYLQSPITTSPSC"
NVRFSTIVRRRAKGAMGLEHIVPNTELRGRLLAGAYHAVVLLDERSAALDGAKRDGTL
ALAGAGACKERRSTQYPSIQGGYERSFSASCPELCSKOSTPMGLSLLPISTSVPDSABESG
CSSCSTPLYDGGGPVELLSFLYLGSAYHASRKDMLDALGITALINVSANCPNHFEGHY
QYKSIPVEDNHKADISSWFNEAIDFIDSIKDAGGRVFVHCQAGISRSATICLAYLMRT
NRYKLDEAFERYKORRSIISPNFSKMQQLLQFESQYLAPHCSAEAGSPAMAVLDRGTS
TTTVRHED TSVYPPRISIISPNFSFGTS
536 C 488 9 462 t
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Rattus norvegicus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                        2100 GGCGCCCAGGAGGCGGGGCGCCGCCCCTGTAGTTGAGCACGCTGAACAGTGCCT 2042
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Submitted (17-JAN-1995) M.Muda, Glaxo Institute for Molecular
Biology, 14 chemin des Aulx, CH-1228 Plan-les-Ouates, Geneva,
SWITZERLAND
                                                                                                                                                                                                                                                                                  130 GGCATCCTGGACGCCGGGGGGCTGCGCGCGCTGCTGCGAGAGCGCGCCCCTCAGTGCCT 188
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Muda,M., Schlegel,W. and Arkinstall,S.
Pathways regulating CL100 gene expression in pituitary cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25; DB 28; Length 1948;
Pred. No. 9.67e-01;
0; Mismatches 17; Indels 0;
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                                                                                                                                                                                           Score 25; DB 28; Length 1912;
Pred. No. 9.67e-01;
0; Mismatches 17; Indels
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R.norvegicus mRNA for dual specificity phosphate.
X84004
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/EC_number="3.1.3.48"
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c1100 gene; protein-tyrosine-phosphatase.

    1948
    /organism="Rattus norvegicus"

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/tissue_type="lung"
/clone_lib="lambda GT10"
/clone="CL100"
164. 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="Sprague-Dawley
/db_xref="taxon:10116"
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164. 135
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Best Local Similarity 71.2%;
Matches 42; Conservative
                                                                                                                                                                                             Query Match 2.8%;
Best Local Similarity 71.2%;
Matches 42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murinae; Rattus.
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179 GGCATCCTGGACGCCGGGGGCTGCGCGCTGCTGCGAGAGCGCGCCGCTCAGTGCCT 237

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CP 2100 GGCGCCCAGGAGGCCGGGCGCCCCCCCCTCTAGITGAGCACGCTGAACAGTGCCC 2042.
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Search completed: Thu Dec 24 17:24:07 1998 Job time: 4464 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

 $\rm n.\,a.$   $\,$   $\,$  n.a. database search, using Smith-Waterman algorithm with gap extension penalties as well as gap opening penalties MPsrch_nna

Thu Dec 24 17:24:26 1998; MasPar time 2466.70 Seconds 654.110 Million cell updates/sec Tabular output not generated. Run on:

>US-08-951-733-13
(1920-2820) from USO8951733.seq (2 of 2)
901
1920 GTCCAGACTCCGCTTCATCC......AGGCCCTGGGTGGCACGGCT 2820
CAGGTCTGAGGCGAAGTAGG......TCCGGGACCCACGTGCGCAA Title:
Description:
Perfect Score:
N.A. Sequence:
Comp:

TABLE default Gap open 30; Gap extend 1 Scoring table:

Dbase 0; Query 0 Nmatch STD:

2275026 seqs, 895388244 bases x 2 Post-processing:

Searched:

Minimum Match 0% Listing first 45 summaries

embl-est55 Database: Database:

1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3 genbank-est107 5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13 10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17 14:gb_est18 15:gb_est19 16:gb_est2 17:gb_est20 18:gb_est2 19:gb_est3 20:gb_est4 21:gb_est5 22:gb_est6 23:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss1 27:gb_gss2 28:gb_gss3 29:gb_gss4

Mean 10.621; Variance 2.221; scale 4.783 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

					COLLINATION		
Doen 1		# C					
No.	Score		Match Length DB	DB	ΩI	Description	Pred. No.
1	161	:	:	24	AA311750	EST182469 Jurkat T-cel	7.58e-249
7	159			ω	AA281296	zt08q02.rl NCI CGAP GC	5.81e-245
m	49	5.4		12	AA754459	97SN1787 Rice Immature	7.23e-42
C 4	47			12	AA754459	97SN1787 Rice Immature	1.31e-38
S	46		247	12	AA754458	97SN1784 Rice Immature	5.39e-37
9 0	44		247	12	AA754458	97SN1784 Rice Immature	8.51e-34
7	33		375	23	AA200728	mul3h09.rl Soares 2NbM	4.00e-17
80	33	3.7	2275 11	11	AF034173	Homo sapiens ntcon2 co	4.00e-17
6	26		343	22	AA098755	T3985 MVAT4 bloodstrea	1.10e-07
10	26		396	13	T26788	T529 Trypanosoma bruce	1.10e-07
11	26		099	11	AF034177	Homo sapiens ntconf co	1.10e-07
12	26		1287	2	AF038250	Homo saniens olone nto	1 100-07

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AF034173 AA848961. AA799774 AF034177 AA619013 W04101	A1022813 A1103459 W69043 AA065279 A1008367	C29002 AI076208 AA555543 AA972885 AA716778	715 715 895 747	W W C V V IO C W IO IO
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## ALIGNMENTS

AA311750 409 bp mRNA EST 19-APR-1997 EST182469 Jurkat T-cells VI Homo sapiens CDNA 5' end, mRNA EST182407 EST3. Homo sapiens Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Wertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;	Defines 1 to 409)  S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Butco, M.D., Serlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Glayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgrafarid, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Moreno-Palanques, R.F., McDonnald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, DF., Ferrie, A., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, L., Weis, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Pillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,	raser, C.M. and Venter, J.C. this assessment of human gene diversity and expression patterns and expression patterns	Marsu upon os militon nucieolides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995) 96026280 Contact: Kerlavage, AR
AA311 EST16 Seque AA311 91964 EST. humar Homo Eukan	Homo.  Adams.  Adams.  Adams.  Bult,  White  Clayt  Gloceg  Gloceg  Gloceg  Born  Moren  Phill  Phill  Phill  Rez W.  Rez W.  Rez W.	Fras( Init:	Natu: 9602(
RESULT 1 LOCUS DEFINITION ACCESSION NID KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL MEDLINE COMMENT

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/organism="Homo sapiens"
/orde="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
                                                                     Email: arkerlavetigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALASA1296 389 bp mRNA EST 14-AUG-1997 2108902.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5', AA281296 g1924194
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 389)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenin.gov
This clone is available royalty-free through LLNL; contact the INSEC Consortium (info@image.llnl.gov) for further information.
Insert Length: 2187 Std Error: 0.00
Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2720 GGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGG 2779
                                                                                                                                                                      1. .409
/organism="Homo sapiens"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
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                      Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                      5 others
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Pred. No. 7.58e-249;
0; Mismatches 0;
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/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
<1. .>409
120 c 133 g 86 t
The Institute for Genomic Research
9712 Medical Center Drive, Rockvill
1913 1018699056
Fax: 3018699423
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Best Local Similarity 100.0%;
Matches 161; Conservative
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AA754459 252 bp mRNA EST 20-JAN-1998
97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
cDNA clone 97SN1787, mRNA sequence.
AA754459
92801165
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/organism="Milyang23"
/rotleivar="Milyang23"
/note="Woctor: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="975NIA87"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa

Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;

Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;

Poales; Poaceae; Oryza.

1 (bases 1 to 252)

Nahm,B.H., Kim,V.R., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,

Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,

Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
National Inst. of Agri. Sci. and Tech, RDA
National Inst. of Agri. Sci. and Tech, RDA
National Science
Tel: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: Mi3 Reverse Primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1980 CGTCGTGGGAGCCAGAACGTTCCGCAGAAAAAAGAGGCCCGAGCGTCTCACCTCGAGGGT 2039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 GTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTA 290
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                                                                                                                                                                                                                          constructed by Bento Soares and M. Fatima Bonaldo." /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 CGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                  /clone-"IMAGE:712562"
/clone_lib="NCI_GGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2040 GAAGGCACTGTTCAGCGTGCTCAACTACGAGCGGGCGCG 2078
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Pred. No. 5.81e-245;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 159; Conservative
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102 c
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Mon Dec 28

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AUTHORS
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/crafilvar="Milyang33"
/cultivar="Milyang33"
/cultivar="Milyang33"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhOI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with XhO I site."
/db.xref="laxon:4530"
/clone="97$N1787"
/clone="97$N1787"
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/clone="97$N1787"
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/clone="15"
/clone="97$N1787"
/clone="16"
/clone="97$N1787"
/clone="16"
/clone="15"
/cl
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AA754459 92801165
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Bukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.

1 (bases 1 to 252)

1 (bases 1 to 252)

1 (bases 1 to 252)

Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
Lee, M.C. and Eun, M.Y.
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Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Fax: 82 311 290 0307
Faxil: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
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                                                                                                                                                                                                                                                                                                                                                                                                            1947 TGACGGCTGCGGCCGGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAG 2006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 VGNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTMWCWBHYNTK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 CTASGWHISINYDVKSSINTWGVTBSYDKSMHGYWCSBBVKYHIKVSTTRATRSYTCVRK 208
                                                                                                                                                                                                                                                                                                                                                                         29 BVWVCVASHGNYMSVHNCIBRGIHCDCKNVNWSIMIWGIVNWBNVSGDWHYWBVBNIKVD 88
                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                  Score 49; DB 12; Length 252;
Pred. No. 7.23e-42;
99; Mismatches 88; Indels
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                                                                                                                                                                                                                                     Query Match 5.4%;
Best Local Similarity 11.0%;
Matches 23; Conservative
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AUTHORS
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AA754458 247 bp mRNA EST 20-JAN-1998 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1784, mRNA sequence. AA754458 92801164
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/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/horte="rectional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="97SN1784"
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Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0301
Fax: Bani: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
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Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
                                                                                                                                                   2695 GGTGAGGTGTCACCAACAAGAAATCATCCACCAACGAGGAGCAGCAGCCCGTCCCGCCGAA 2636
                                                                                                                                                                                                                                                                                                                                                                                                     2635 TCCCCGCAAACAGCTTGTTCTCCATGTCGCCGTAGCACAGGCTGCAGAGCAGCGTGGAGA 2576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
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                                                               Gaps
                                                                                                                                                                                                                                     83 BNTKVDVGNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTMWCW
                                                                                                                                                                                                                                                                                                                                                     143 BHYNTKCTASGWHTSTNYDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVSTTRATRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 YTCVRKYCVMWMTKKVVKKYHVVBBGCHBTDSKCKTMWMTNKHVMTSTTD 252
      Length 252;
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Ouery Match 5.2%; Score 47; DB 12; Length 252 Best Local Similarity 10.0%; Pred. No..1.31e-38; Matches 23; Conservative 107; Mismatches 100; Indels
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Pred. No. 5.39e-37;
92; Mismatches 89; Indels
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/dev_stage="S days after pollination"
/lab_host="E. coli SOLR"
/lab_host="E. 21 g 34 t 169 ot)
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Best Local Similarity 12.6%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Eun M.Y.
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윱 ö 셤 ò ద ö ORGANISM

REFERENCE AUTHORS

ACCESSION KEYWORDS SOURCE

RESULT

TITLE JOURNAL COMMENT

FEATURES

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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Galsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
AA200728 375 bp mRNA EST 19-FEB-1997 mul3h09.rl Soares 2NbMT Mus musculus cDNA clone 639329 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7el: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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Pred. No. 4.00e-17;
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Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 361.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares 2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090
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/dev_stage="4 weeks"
/lab_host="DH10B"
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Local Similarity 75.4%;
Les 49; Conservative
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1 (bases 1 to 375)
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AA200728
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/organism="Oryza sativa"
/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/Not: Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="Laxon:4530"
/clone="9768M1784"
/clone="9768M1784"
/clone="15-Rice. Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/lab_host="E. coli SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA754458 247 bp mRNA EST 20-JAN-1998 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1784, mRNA sequence.
AA754458 92801164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Bubryophyta; Tracheophyta; seed plants; Magnoliophyta; Lillopsida;
Poales; Poaceae; Oryza.
1 (bases 1 to 247)
1 (bases 2 to 247)
1 (bases 2 to 247)
1 (bases 3 to 247)
1 (bases 4 to 247)
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Mational Inst. of Agr1. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fmax: 82 331 290 0307
Fmail: myeun&sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yonghin, Rorea. 449-728 bhnahm@bioserver.myongji.ac.kr
Location/Qualifiers
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                                                                                                                                                                                                          RCINDRGYCNYTASDNGISATKRVIGYDKTDSDCGGGCWRKVIYGSSBYBRCGVNVMVRT 198
                                       79 TBYYSWNVDINIGGIGVGKTIVNVHSGWNNRCSNSVVYVWBIAYCDYBHYBDRANHVDDT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 8.51e-34;
60; Mismatches 36; Indels
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Best Local Similarity 12.7%;
Matches 14; Conservative
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LOCUS AF034173 2275 bp mRNA EST 22-DEC-1997 DEFINITION Homo sapiens ntcon2 contig mRNA, partial sequence, mRNA sequence.
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Length 375;

BASE COUNT

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Tel: 3193356918
Fax: 3193356764
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                                                                                                                                                                                                    Unpublished

2 (bases 1 to 2275)

Tripodis,u. and Ragoussis,J.

Direct Submission

Submitted (13-NOV-1997) Division of Medical and Molecular Genetics,

Guy's Hospital, 7th floor, Guy's Tower, London SE1 9RT, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 343)
Jakeng-A., Donelson,J.E. and Majiwa,P.A.O.
Generation of expressed sequence tags as physical landmarks in the
genome of Trypanosoma brucei
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Trypanosoma brucei rhodesiense
Eukaryotae; mitochondiial eukaryotes; Euglenozoa; Kinetoplastida;
Trypanosomatidae; Trypanosoma.
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T3985 MVAT4 bloodstream form of serodeme WRATatl.1 Trypanosoma
brucei rhodesiense cDNA 5' similar to gi|477308|pir||A48583
ribosomal protein S11, mRNA sequence.
AA098755
g1644707
                                                                                 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhin; Hominidae; Homo. (fases 1 to 2275)
Tripodis, N. and Ragoussis, J. Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 11; Length 227 Pred. No. 4.00e-17; 47; Mismatches 25; Indels
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International Livestock Research Institute
P.O. Box 30709, Nairobi, Kenya
Tel: 254-2 630743
Fax: 254-2 631499
Email: p.majiwaecgnet.com
Seq primer: T3 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        /map="opin...
/clone="ntcon2 contig"
/tissue_type="liver; brain"
/dev_stage="fetus"
/note="similar to Br140"
a 619 c 470 g 599.t
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                                                                                                                                                                                                                                                                                                                            1. .2275
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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                                                                                                                                                                                                                                                                                                                                                                                                   /map="6p21.3"
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Best Local Similarity 13.3%;
Matches 11; Conservative
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                                                                    Homo sapiens
AF034173
q2707735
                                                                                                                                                                                       boundary
                                                    human.
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AUTHORS
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/note="vector: Lambda ZAP II (Stratagene); Site_1: EcorI; Site_2: XhoI; The mRNA was purified from a cloned population of bloodstream trypanosomes reexpressing the MVAT4 metacyclic variant surface glycoprotein (VSG). A unidirectional oligo dT-primed EcoRI/KhoI cDNA library was constructed in lambda ZAP II (Stratagene)."

/db_xref="taxon:31286"
/clone_lib="MVAT4 bloodstream form of serodeme WRATatI.1"
/I c 86 g 82 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         African trypanosome primer=T3 primer library=MVAT4 bloodstream form of serodeme WRATat1.1 vector=Lambda ZAP II (Stratagene)
Rsitel=EcorI Rsite2=XhoI The mRNA was purified from a cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           John Donelson's Laboratory
Howard Hughes Medical Institute
300 EMRB, Dept. of Biochemistry, University of Iowa, Iowa City, IA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       population of bloodstream trypanosomes reexpressing the MVAT4 metacyclic variant surface glycoprotein (VSG). A unidirectional oligo dT-primed EcoRI/XhoI cDNA library was constructed in lambda ZAP II (Stratagene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trypanosoma brucei rhodesiense
Eukaryotae, mitochondrial eukaryotes; Euglenozoa; Kinetoplastida;
Trypanosomatidae; Trypanosoma; Trypanosoma brucel.
1 (bases 1 to 396)
El-Sayed,N.M.A.
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Homo sapiens ntcon6 contig mRNA, partial sequence, mRNA sequence.
AF034177
g2707739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126788 396 bp mRNA EST 06-NOV-1995
protein S11 homolog.
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                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                        Length 343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           237 CCAGACGCCGTCAATGAGAACATTCGCACGGCCTCCAAGAAGCACGT 284
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Pred. No. 1.10e-07;
0; Mismatches 11; Indels
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Pred. No. 1.10e-07;
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/organism="Trypanosoma
<1. .>396
1 .101 c 87 g
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                                                                                                                                                                                                                                                                                                                                   Query Match 2.9%;
Best Local Similarity 77.1%;
Matches 37; Conservative
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Best Local Similarity 77.1%;
Matches 37; Conservative
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ORGANISM

KEYWORDS

AUTHORS TITLE

REFERENCE

JOURNAL REFERENCE

AUTHORS

source

FEATURES

JOURNAL

BASE COUNT

ORIGIN

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Tripodis. N. and Ragoussis, J.

Tripodis. N. and Ragoussis, J.

Direct Submission

Submitted (13.00v-1997) Division of Medical and Molecular Genetics, Guy's Hospital, 7th floor, Guy's Tower, London SEI 9RT, UK

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAMSTAGI 301 bp mRNA EST 30-APR-1998
EST191723 Normalized rat lung, Bento Soares Rattus sp. cDNA clone
AA848961
G29335501
                                                                                                                                  AF034173 2275 bp mRNA EST 22-DEC-1997
Homo sapiens ntcon2 contig mRNA, partial sequence, mRNA sequence.
AF034173
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Eodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 301)

Lee, N. H., Glodek, A., Chandra, I., Mason, T. M., Quackenbush, J.,

Kerlavage, A. R. and Adams, M.D.

Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1483 RWKRRKGRRKRMTGMYKRMYRAMMAMCAMMACWWYYWKMRGMKKCWKYRKYTSTYY 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2703 GIGGGTGAGGTGAGGTGTCACCAACAAGAAATCATCCACCAAAGGAGGAGCAGCCGTC 2644
                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 227:)
Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately
centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
boundary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26; DB 11; Length 2275;
Pred. No. 1.10e-07;
37; Mismatches 17; Indels
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/tissue_type="liver; brain"
/dev_stage="fetus"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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Best Local Similarity 10.0%;
Matches 6; Conservative
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456 GSAGVTVNHHDWS 468
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Unpublished
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2 (bases 1 to 660)
2 ripodis,N. and Ragoussis,J.
Direct Submission
Submitted (13-NoV-1997) Division of Medical and Molecular Genetics,
Guy's Hospital, 7th floor, Guy's Tower, London SEI 9RT, UK
Location/Qualifiers
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1287)
1 ripodis, N. and Ragoussis, J.
Direct Submission
Submitted (12-DEC-1997) Division of Medical and Molecular Genetics, Guy's Hospital, 7th floor, Guy's Tower, London SEI 9RT, UK
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Homo sapiens clone ntcon9 mRNA, partial sequence, mRNA sequence.
AF038250
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                                                            Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 660)
Tripodis,N. and Ragoussis,J. Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /may-up.r...
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/note="similar to CutA"
/note="similar to CutA"
/note="similar to CutA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 660;
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Best Local Similarity 26.0%; Pred. No. 1.10e-07;
Matches 19; Conservative 29; Mismatches 25; Indels
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Pred. No. 1.10e-07;
29; Mismatches 11; Indels
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/note="sinilar to HSRP20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%;
Best Local Similarity 16.7%;
Matches 8; Conservative
                                            Homo sapiens
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DEFINITION ACCESSION

RESULT

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KEYWORDS SOURCE

REFERENCE

AUTHORS

JOURNAL

FEATURES

BASE COUNT

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US-08-951-733-13-03.rst

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AA799774 318 bp mRNA EST 30-APR-1998 EST189271 Normalized rat heart, Bento Soares Rattus sp. cDNA clone RAFAF18 3' end, mRNA sequence. AA799774 92862729
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Rattus sp.
Bukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 318)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Rerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
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/organism="Rattus sp."

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/clone=lib="Normalized rat heart, Bento Soares"

a 113 c 94 g 57 t
                                                                                                                                                                                                                                                                                                                                                                                ). .301
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/orde="Organ: lung; Vector: pT7T3Pac; Site_1: ECORI;
Site_2: Not!"
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/clone="RLUAI44"
/clone_iib="Normalized rat lung, Bento Soares"
a 104 c 90 g 54 t
                                                                                                                                                                                                                                                                                                                                                            104 AGGCACTGAGCGGCGCGCTCTCGCAGCAGCGCGCGCGCCCCCCGGGCGTCCAGGATGCC 162
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Pred. No. 1.91e-06;
0; Mismatches 17; Indels 0; Gaps
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The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
9713, Medical Center Drive, Rockville, MD 20850, USA
9713, Medical Center Drive, Rockville, MD 20850, USA
Fax: (301)-838-3529
Fax: (301)-838-3529
Email: nhleefigr.org
Seq primer: MJ-21
Coation/Qualifiers
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Pred. No. 1.91e-06;
0; Mismatches 17; Indels
                   Location/Qualifiers
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Best Local Similarity 71.2%;
Matches 42; Conservative
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Best Local Similarity 71.2%;
Matches 42; Conservative
Seq primer: M13-21
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Thu Dec 24 18:30:54 1998; MasPar time 274.67 Seconds 446.298 Million cell updates/sec Run on:

Tabular output not generated.

>US-08-951-733-13
(1920-2820) from USO8951733.seq (2 of 2)
901
1920 GTCCAGACTCCGCTTCATCC......AGGCCCTGGGTGGCACGGCT 2820
CAGGTCTGAGGCGAAGTAGG......TCCGGGACCCACGTGCCGA Description: Perfect Score: N.A. Sequence: Comp:

TABLE default Gap open 30; Gap extend 1 Scoring table:

188442 seqs, 68026449 bases x 2 Searched:

Dbase 0; Query 0

STD :

Nmatch

Minimum Match 0% Listing first 45 summaries Post-processing:

| Spart | 2.part | 3.part | 3.part | 5.part | 5.part | 2.part | 2.part | 2.part | 2.part | 2.part | 2.part | 3.part | 3. n-geneseq32 Database:

Mean 8.771; Variance 5.114; scale 1.715 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

o.	12	11	10	10	60	80	07	07	07	07	07	
Pred. No.	7.51e-12	3.02e-11	1.20e-10	4.75e-10	7.23e-	2.78e-08	1.06e-07	1.06e-07	1.06e-07	1.06e-07	1.06e-07	FO-000 V
Description	ligonucleotide probe	ligonucleotide probe	dase substituted E.co	dase substituted E.co	Generic DNA sequence	Seneric DNA sequence	Seneric DNA sequence			Seneric DNA sequence		Concinc AMA concent
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* Query Watch Length DB	91	91	204	204	114	114	114	114	114	114	114	117
Query Match	4.8	4.7	4.6	4.4	4.2	4.1	4.0	4.0	4.0	4.0	4.0	ص ~
Score	43	42	41	40	38	37	36	36	36	36	36	
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2 070470 GG 2 070458 GG 070468 GG 070468 GG 070465 GG 070471 GG 070471 GG 070471 GG 070473 GG 07	ore 4
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darding dardin	Similarity 4; Conserv
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Matches
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C. Random point mutations were introduced into the alpha fragment of E coil beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3 ends generated in this way are used as primers for reverse transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which centre also p80575.

C. Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
WPI; 88-279927440.
Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-Nov-1990 (first entry)
asse substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                            7 ggcgssvhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvvhhvhyhvyvsv 60
                                                                                                                                                                                                                Claim 3; Page 14; 23pp; English.
Oligonuclectide probe MK14-A consists of nucleotides 5-95 of 1 (051735). It hybridized to all spp. of mycobacteria tested, lorss reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also 031735-45 and 051747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T:
                                                                                                                                                                                  nseq
                      31-WAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                      (BECT ) BECTON DICKINSON CO.
Shank DD. Spears PA;
WPI; 93-378844/48.
New Oligo:nucleotide probes specific for Mycobacteria - used
detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                         Length 91;
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Pred. No. 3.02e-11;
45; Mismatches 6;
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/*tag= a
/function=multiple cloning site
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 BP.
                                                                                                                                                                                                                                                                                                                        4.78;
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Conservative
standard; cDNA; 91
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/*tag= b
                                                                                                    01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
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Matches 3; Conser
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                                                                          Synthetic.
EP-571911-A.
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Score 41; DB 1; Length 204;

4.68;

Query Match

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SUPPRINTINGS:

30-APR-1988; 105163.

81205 SUOMEN SOKERI OY.

1 Entroducing random point mutations into nucleic acods.

Introducing random point mutations into nucleic acods.

1 Introducing random point mutations into nucleic acods.

1 Introducing random point mutations into nucleic acods.

2 Introducing random point mutations into nucleic acods.

2 Introducing random point mutations were introduced into the alpha fragment of misincorporation, completion of molecules and screening.

2 Introducing int mutations were introduced into the alpha fragment of paralogomerate a popn of Introduced into the alpha fragment of angle stranded template and an oligonucleotide was obtained as a single stranded template and an oligonucleotide was bybridised to it to generate a popn of DNA molecules which terminate at all the sessible nucleotide positions which terminate at all reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which
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                                                                                                                                                                                                                    aaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncncccbnnhvchnvhbnnh 169
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070465;
05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
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   Pred. No. 1.20e-10;
58; Mismatches 59; Indels
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/*tag= a
/function=multiple cloning site
187..204
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1973 ATGTTCACAATCGGCCGCAGCCCG 1950
                                                                                                                                                                                                                                                                                                                                      rnwayvrhdarrddvhccvchccg 193
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Similarity 8.2%;
9; Conservative
Best Local Similarity 18.8%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-1990 (first entry)
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Best Local Similarity
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ID Q7
AC Q7
DT 05
DE G6
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18-AUG-1994.
01-FEB-1994; U
01-FEB-1993; U
30-DEC-1993; U
                                                                            01-FEB-1993;
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05-APR-1995
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Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PT screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure; Page 35; 25pp; English.

C 070465 is a generic DNA Sequence used to generate random TSAR (Totally

C 070465 is a generic DNA Sequence used to generate can also be

represented as follows: X(NNB) [GGC) (NNB) 11Z (NNB) 14 (TGC) (NNB) 37. X

and Y are flanking restriction sites (X is not the same as Y) that are

conter specified further. Other generic sequences are shown in G7046-68.

C other specified further or generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in R65151-54. TSARs are concatenated by these generic sequences are shown in C R65151-54. TSARs are concatenated by these generic sequences are shown in GR6151-64. TSARs are concatenated by these generic sequences are shown in C R65151-64. TSARs are concatenated by these generic sequences are shown in GR6151-64. TSARs are concatenated by these generic sequences are shown in C chairly for a ligand and a second effector peptide portion that is chairly be between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues correspondence or comparison and so replace the function of macromolecules, eg.

C radioisotope, peptide, toxin or enzyme, to the specific target or on the container methods of hybridoma formation of macromolecules, eg.

C complex methods of hybridoma formation or in vivo antibody or production. The TSARs are easily characterised and have designed and have designed and page and and recomblex methods of hybridoma formation or in vivo antibody.
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TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
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effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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/note= "this sequence represents 'Z'; Z can be
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                                                                           /*tag= a
/note= "this sequence represents '2'; 2
sequence of 6, 9 or 12 nucleotides (see
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33; Mismatches 73
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6;
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                                              Location/Qualifiers
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                                                                                                                                                                                                                               NORTH CAROLINA.
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07-APR-1995 (first entry)
Generic DNA sequence to ger
                                                                                                                         comments)"
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31-JAN-1994;
                                                            misc_feature
                                                                                                                                                                                    01-FEB-1993;
                                                                                                                                                                                                                                                 Fowlkes DM,
                               Synthetic.
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Matches
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FOWINGS DM, Kay BK;

DR WPI: 94-279739/34.

DR WPI: 94-279739/34.

DR WPI: 94-279739/34.

PT Identifying proteins or peptide(s) which bind a ligand - by

Identifying proteins or peptide(s) which bind a ligand - by

PT Screening a recombinant vector library expressing fusion proteins

PT Comprising a binding domain and an effector domain

Disclosure; Page 35; 255pp; English.

CQ 070469 is a generic DNA Sequence used to generate random TSAR peptide

CC THIS generic formula can be represented as follows: X(TGC) (NNB)10-

CT GC)(NNB)52(NNB)2(TGC)(NNB)14(TGC)Y. X and Y are flanking restriction

CC THS generates peptides that are cloverlaed in structure. Other

CC Greated by these generic sequences are shown in R65150-54. TSARs are

CC Goncatenated by these generic sequences are shown in R65150-54. TSARs are

CC Goncatenated beterofunctional proteins or peptides, comprising at least

CC Goncatenated beterofunctional proteins or peptides, comprising at least

CC Goncatenated beterofunctional proteins or peptides comprising the content of a second effector peptide portion that is chemically or biologically active morphisms or comprising at least

CC The Oligonuclectides are also designed so that the expressed peptide

CC CONTENT OF A CONTENT COMPINED THAT IN THE TSARS OF COMPINED THE CONTENT OF THE CC CONTENT OF THE CONTENT OF THE CONTENT OF THE CC CONTENT OF THE CONTENT OF THE CONTENT OF THE CC CONTENT OF THE CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             //outs "this sequence represents '2'; 2 can sequence of 6, 9 or 12 nucleotides (see comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 12; Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 2.78e-08;
32; Mismatches 72; Indels
of 6,9 or 12 nucleotides (see
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C)
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Sequence 114 BP; 0 A; 4 C
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Q70467 standard; DNA; 114 BP.
                                                                                                                                                                                                                        30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Ray BK;
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                                     comments)
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sednence
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US-176500.
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US-176500.
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Matches 7; Conser
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                                                                                                                                                                                                                                                          2442 CGAGCAGAGCTCCTCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCTACGCTT 2501
                                                                                                                                                                                                                                                                                                                                    Generic DNA sequence to generate a random TSAR petide library.

TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss. Synthetic.
                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins
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                                                                                                                                                                                                                                                                                    2502 CATGTGCCACCCCGCGCGCGCATCAGGGGCAAGTCCTACGTCCCAGTGCCAG 2553
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                                                                                                                                                                                                                                                                            Length 114;
                                                                                                                                                                                                                                     74; Indels
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                                                                                                                                                                                                                             Pred. No. 1.06e-07;
34; Mismatches 74
                                                                                                                                                                                                                         DB 12;
                                                                                                                                                                                                                         Score 36;
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1994.
01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UNC) UINV NORTH CAROLINA.
FOWNKES DM, KAY BK;
WPI; 94-Z79739/34.
                                                                                                                                                                                                                                                                                                           070468 standard; DNA; 114 BP. 070468; 05-APR-1995 (first entry)
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                              Similarity 3.6%;
4; Conservative
                                                                                                                                                                                                                       4.0%;
                                                                                                                                                                                                                                                                                                                                                                              . 60
            94-279739/34.
                                                                                                                                                                                                                             Best_Local Similarity
Matches 4; Conse
                    WPI; 94-279739
P-PSDB; R65153
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PT comprising a binding domain and an effector domain

Bisclosure; Page 35; 255pp; English.

CTO468 is a generic DNA sequence used to generate random TSAR (Totally
CY0468 is a generic DNA sequence used to generate random TSAR (Totally
CYNTHELIC AFfinity Reagents) peptides.This generic formula can also be
come to specified further. Other generic sequences are shown in Q70466.68.

CC cher specific peptides generated by these generic sequences are shown in
CC K65151-54. TSARs are concatenated heterofunctional proteins or peptides,
CC omprising at least two functional regions. - a binding domain with
CC Affinity for a ligand and a second effector peptide portion that is
CC chemically or biologically active. They may further comprise a linker
CC femically or biologically active. They may further comprise a linker
CC finity for a ligand and a second effector peptide portion that is
CC femically or biologically active molety est are also designed so
CC in, or flanking, the unpredicted or variant residues. These residues
CC offer some degree of conformational rigidity to the peptides. The TSARs
CC confer some degree of conformational rigidity to the peptides.
CC deliver a chemically or biologically active molety, eg. metal lon,
CC addiostope, peptide, toxin or enzyme, to the specific target or on the
CC coll. They can also replace the function of macromolecules, eg.
CC concorders methods of hybridoma formation or in vivo antibody
CC concorder and reasily characterised and have designed activity
CC concorder.
CC complex methods of hybridoma formation or in vivo antibody
CC concorder.
CC complex methods of hybridoma formation or an expectation of a screening process.
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070466 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides.This generic formula can also be represented as follows:X(NNB)1(TGC)(NNB)10(TGC)2(NNB)4Z(NNB)8(TGC)(NNB)9Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2055 CGIGCICAACIACGAGCGGGCGCGCCCCCGGCCICCTGGGCGCCTCTGTGCTGGGCCT 2114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generic DNA sequence to generate a random TSAR-9 petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 banbanbanbanbanbtgcanbanbanbanbanbanbanbanbanbanbanb 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
1.06e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36;
Pred. No.
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWINES DM, KAY BK;
WPI: 94-279739/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q70466 standard; DNA; 114 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.0%;
Similarity 3.6%;
4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 BP;
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05-APR-1995
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cc q70466-68. Other specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a clinker peptide between the 2 domains. The oligonuclocides are also designed so that the expressed peptide contains 2 or 4 cysteine residues confers some degree of conformational rigidity to the peptides. Cc residues confers some degree of conformational rigidity to the peptides. The TSARs or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal contains a chemically or biologically active molety, eg. metal contains peptide, toxin or ensyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing cc direct and rapid detection in a screening process.
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2567 GCTCCATCCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGT 2626
                                                                     genabanbanbanbanbanbanbanbanbtgetgenabanbanbanbanannan 64
                                     Gaps
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                                                                                                                                                                   2627 TIGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGATTTC 2676
                                                                                                                                          65 nbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnb 114
Length 114;
               Pred. No. 1.06e-07;
31; Mismatches 71; Indels
Score 36; DB 12; Pred. No. 1.06e-07;
4.0%;
                                   Conservative
         Best Local Similarity
Matches 8; Conser
Query Match
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Transference of the complication of peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain proteins binding domain and an effector domain proteins of processing binding domain and an effector domain bisclosure; Page 35; 255pp; English sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be spresented as follows: X(NNB)16(TGC)(NNB)16(TGC)(NNB)17. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68. Other specified further other generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with a finitity for a ligand and a second effector peptide portion that is chemically or biologically active They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed that the expressed peptide contains 2 or 4 cysteine residues positioned
                                                                                  Generic DNA sequence to generate a random TSAR petide library. TSAR: totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                                                                                                                                                                                                                                  /*tag= a
/note="this sequence represents 'Z'; Z can be
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                                                                                                                         Location/Qualifiers
                   Q70467 standard; DNA; 114 BP. Q70467;
                                                                                                                                                                                                                                                                                                                                                                                               30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWIKES DM, RAY BK;
WPI; 94-279339/34.
                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                          U00977.
US-013416.
US-176500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R65153
                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994;
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                                                             05-APR-1995
Generic DNA
                                                                                                                                                                                                                                                                                                                   WO9418318-A
                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
RESULT
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in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compans. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
                                                                                                                                                   ö
                                                                                                                                                                                       2610 GTCGCCGTAGCACAGGCTGCAGAGCAGCGTGGAGGATGGAGCCCTGCGGGATCCCCTG 2551
                                                                                                                                                                    Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                   Gaps
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                                                                                                                            Length 114;
                                                                                                                                      Pred. No. 1.06e-07;
33; Mismatches 70; Indels
                                                                                                                                                                                                                              2550 GCACTGGACGTAGGACTTGCCCCTGATGCGCACGGCGTGGTGGCAC 2505
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/note= "encoded by Z (see comments)"
                                                                                                                            DB 12;
                                                                                                                            Score 36;
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                           Query Match 4.0%;
Best Local Similarity 2.8%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                               JT 11
Q70470 standard; DNA; 114
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                                                                                                                                                                                                                                                                                   Q70470;
10-APR-1995
                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure; Page 35; 255pp. English.

COMPAGE 1s a generic DNA Sequence used to generate random TSAR peptide

COMPAGE 1s a generic DNA Sequence used to generate random TSAR peptide

CTGC)(NNB)6Z(NNB)2(TGC)(NNB)14(TGC)Y. A and Y are flanking restriction

SITES (X is not the same as Y) that are not specified further. This

CC STECS (NNB)6Z(NNB)2(TGC)(NNB)14(TGC)Y. A and Y are flanking restriction

SITES (X is not the same as Y) that are cloverleaf in structure. Other

CC Generic Sequences are shown in Q70465-68. Other specific peptides

CC Generated by these generic sequences are shown in R65150-54. TSARs are

CONCATENATED TREADING - a binding domain with affairty for a ligand and

CA SECOND Effector peptide portion that is chemically or biologically

CC A CONTAINS 2 or 4 Cysteine residues positioned in, or flanking, the

CC CONTAINS 2 or 4 Cysteine residues positioned in, or flanking, the

CC CONTAINS 2 or 4 Cysteine residues positioned in, or flanking, the

CONTAINS 2 or 4 Cysteine residues positioned in, or flanking, the

CONTAINS 3 or 4 Cysteine residues. These residues confer some degree of

CONTAINS 4 or 4 Cysteine residues. The TSARs or compsns. comprising

CONTAINS 5 or 4 Cysteine residues positioned in, or flanking, the

CONTAINS 5 or 4 Cysteine residues or the second also replace

CC enzyme, to the specific target or on the cell. They can also replace

CC enzyme, to the specific target or on the cell. They can also replace

CC enzyme, to the specific target or on the cell. They can also desides

CC CONTAINS 6 machonic edge or complex methods of hybridoma

CC CONTAINS 7 or A Cysteine designed and bave as a saily

CC Charaction or in vivo antibody production. The TSARs are easily
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                                                                                                                       2625 CAGCTTGTTCTCCATGTCGCCGTAGCACAGGCTGCAGAGCTGGAGCC 2566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2616 CTCCATGTCGCCGTAGCACAGGCTGCAGAGCAGCGTGGAGAGGATGGAGCCCTGCGGGGAT 2557
                                                                                        3 bnabanbanbcacanbanbanbanbcacanbanbanbanbanbanbanbanbanannan 62
                                                                                                                                                                                                                                                                                                                                                                                            Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                                                  Gaps
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/*tag- a /
hote= "this sequence represents '2'; Z can be sequence of 6,9 or 12 nucleotides (see
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Pred. No. 4.00e-07;
32; Mismatches 72; Indels
    Length 114;
Score 36; DB 12; Length 114
Pred. No. 1.06e-07;
30; Mismatches 66; Indels
                                                                                                                                                                                                                                2565 CTGCGGGATCCCCTGGCACTGGACGTAGGACTTGCCCCTGATGC 2522
                                                                                                                                                                                     63 bnnbnnbnnbnnbnnbcacnnbnnbnnbnnbnnbnnbnnbc 106
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Q70469 standard; DNA; 114 BP.
Q70469;
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
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                                                  Conservative
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Best Local Similarity
  Query Match
Best Local Similarity
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01-FEB-1993;
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Treating proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins promprising a binding domain and an effector domain bisclosure; Page 36; 255pp; English, and sequence used to generate random TSAR (Totally Disclosure, Page 36; 255pp; English, This generic formula can also be synthetic Affinity Reagents) peptides This generic formula can also be represented as follows: X(NNB)4(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)(NNB)8(CAC)
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10-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
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                                                                                                                                                                                                                     Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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                              Length 114;
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Pred. No. 1.49e-06;
30; Mismatches 68; Indels
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/note= "encoded by Z (see comments)"
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Q70470 standard; DNA; 114 BP.
Q70470;
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UXNC-) UNIV NORTH CAROLINA.
FOWlkes DM, RAY BK;
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Similarity 7.5%;
8; Conservative
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WPI; 94-279739/34.
P-PSDB; R58378.
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Per Forbaik KASAS.

Tenetifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain

Tenestising a binding domain and an effector domain

Disclosure: Page 36; 255pp; English.

O70472 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affilinty Reagents) peptides. This generic formula can also be represented as follows: X(NNB)[(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(CAC)(NNB)(N
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/note= "this sequence represents '2'; Z can be a
sequence of 6, 9 or 12 nucleotides (see
comments)"
effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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Pred. No. 1.49e-06;
30; Mismatches 71; Indels
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(UVNC) UNIV NORTH CAROLINA.
FOWNKES DM, KAY BK;
WPI; 94-279739/34.
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Best Local Similarity 9.8%;
Matches 11; Conservative
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05-APR-1995 (first entry)
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US-176500.
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01-FEB-1994; U00977.
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                                                       Synthetic.
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Treatming a recombinant vector library expressing fusion proteins processing a recombinant vector library expressing fusion proteins processing a binding domain and an effector domain proteins by sociative; PSG 525pp; English.

C 070468 is a generic DNA sequence used to generate random TSAR (Totally CTO 070468 is a generic DNA sequence used to generate formula can also be represented as follows: X(NNB)11(TGC)(NNB)5Z(NNB)7C(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generated by these generic sequences are shown in Q70466.68.

C other specific peptides generated by these generic sequences are shown in R65151-54. TSARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is comprising at least two functions. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues conference of conformational rigidity to the peptides. The TSARS confers some degree of conformational rigidity to the peptides. The TSARS corrections or peptides to an also replace the function of macromolecules, eq. monoclonal or polyclonal antibodies and therefore circumvent the need correction. The TSARs are easily characterised and have designed activity correction. The TSARs are easily characterised and have designed activity sequence 114 BP; 0 A; 2 C; 2 C; 2 C; 2 C;
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Pred. No. 1.49e-06;
34; Mismatches 75; Indels
                                                                                                                                                                                  Identifying proteins or peptide(s) which bind a ligand screening a recombinant vector library expressing fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: Thu Dec 24 18:37:53 1998 Job time : 419 secs.
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.larity 2.7%;
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01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UINC-) UNIV NORTH CAROLINA.
                                                                                                      Fowlkes DM, Kay BK; WPI; 94-279739/34.
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Best Local Similarity
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2171 21 US-08-846- Sequence 100, Applicat 3496 23 US-09-042- Sequence 1, Applications 255 22 US-08-911- Sequence 54, Applications 22 US-08-912- Sequence 54, Applications 22 US-08-912- Sequence 54, Applications 389 21 US-08-846- Sequence 62, Applications 389 21 US-08-846- Sequence 62, Applications 389 22 US-08-81- Sequence 62, Applications 389 22 US-08-91- Sequence 62, Applications 389 22 US-08-91- Sequence 62, Applications 389 22 US-08-91- Sequence 63, Applications 389 22 US-08-91- Sequence 8, Applications 383 16 US-08-654- Sequence 8, Applications 383 16 US-08-446- Sequence 8, Applications 240 US-08-446- US-08-4	57 6.3 38316 US-08-446 Sequence 8, Applicatio 5 6.3 38317 US-08-451 Sequence 8, Applicatio 5 6.3 38317 US-08-451 Sequence 8, Applicatio 5 6.3 38316 US-08-446 Sequence 8, Applicatio 5 6.1 38316 US-08-451 Sequence 8, Applicatio 5 6.1 38315 US-08-311 Sequence 8, Applicatio 5 6.1 38315 US-08-311 Sequence 9, Applicatio 5 6.1 38315 US-08-911 Sequence 328, Applicatio 5 6.1 383 US-08-911 Sequence 538, Applicatio 5 6.1 383 US-08-911 Sequence 538, Applicatio 5 6.1 383 US-08-912 Sequence 538, Applicatio 5 6.1 383 US-08-911 Sequence 53, Application 5 5.9 239 22 US-08-911 Sequence 53, Application 5 5.9 239 22 US-08-911 Sequence 53, Application 5 5.9 239 22 US-08-911 Sequence 14, Application 5 5.9 239 22 US-08-911 Sequence 53, Application 5 5.9 239 20 US-08-911 Sequence 53, Application 5 5.9 239 25 US-08-911 Sequence 53, Application 5 5.9 230 25 US-08-911 Sequence 53, Application 5 5 5 5 5 5 5 5 5 5 5 5 5 5	SULT 1 US-08-951-733- XXXXXX SEQUENCE 13, R SEQUENCE 13, R GENERAL INFOR APPLICANT: TITLE OF IT NUMBER OF S CORRESPONDE	CC STREET: One Amgen Center Drive CC STREET: CA COUNTRY: USA CC STREET: Thousand Oaks CC STREET: Thousand Oaks CC COUNTRY: USA CC COUNTRY: USA CC CONFUTER READBLE Floppy disk CC CONFUTER PRABBLE FORM: MEDIUM TYPE: Floppy disk CC CONFUTER: DAY COMPATIBLE PO-DS/MS-DOS CC CONFUTER: DAY CONFUTER: USA CONFUTER
######################################	n.a. database search, using Smith-Water p extension penalties as well as gap ope u Dec 24 18:38:12 1998; MasPar time 155 generated. S-08-951-733-13 1200 GTCCAGACTCGCTTCATCCAGGCC CAGGTCTGAGGCGAAGTAGGTCCGG	SID:	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  SUMMARIES  Result  Ouery  No. Score Match Length DB ID  1 100.0 2848 22 US-08-951- Sequence 13, Applicatio 0.00e+00 2 901 100.0 3798 22 US-08-951- Sequence 19, Applicatio 0.00e+00 4 901 100.0 4015 21 US-08-951- Sequence 1, Applicatio 0.00e+00 6 901 100.0 4015 21 US-08-912- Sequence 1, Applicatio 0.00e+00 6 901 100.0 4015 21 US-08-912- Sequence 1, Applicatio 0.00e+00 6 901 100.0 4015 21 US-08-913- Sequence 1, Applicatio 0.00e+00 7 029 22 US-08-913- Sequence 1, Applicatio 0.00e+00 100.0 4029 21 US-08-913- Sequence 173, Applicatio 0.00e+00 100.0 4029 21 US-08-913- Sequence 173, Applicatio 0.00e+00 10 508 56.4 2176 22 US-08-913- Sequence 35, Applicatio 0.00e+00 11 508 56.4 2176 22 US-08-913- Sequence 36, Applicatio 0.00e+00 11 508 56.4 3855 22 US-08-913- Sequence 36, Applicatio 0.00e+00 11 508 56.4 3855 22 US-08-913- Sequence 36, Applicatio 0.00e+00 11 508 56.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 508 56.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 508 56.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 508 56.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 508 56.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 508 56.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 508 56.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 508 56.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 508 50.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 508 50.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 508 50.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 508 50.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 508 50.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 508 50.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 508 50.4 3855 22 US-08-913- Sequence 100, Applicatio 0.00e+00 11 500 500 500 50

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STATE: CA
COUNTRY:
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                                                                                                       Score 901; DB 22; Length 2848;
Pred. No. 0.00e+00;
0; Mismatches 0; Indels 0
TELEFAX: (805) 499-8011
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2848 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE 2848 BP; 437 A; 978 C; 945 G; 488 T; 0 OTHER.
                                                                                                       Match 100.0%;
Local Similarity 100.0%;
les 901; Conservative
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                                                                                                                                                              APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVEXTION: NOVEL GENES ENCODING TELOMERASE PROTEINS
NUMBER OF SEQUENCES: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTIAN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,733
FILING DATE: 16-OCT-1997
CLASSIFICATION: 455
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/873,039
FILING DATE: 11-70N 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,189
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: OLESKI, Nancy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
SEQUENCE 3798 BP; 613 A; 1310 C; 1213 G; 662 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 901; DB 22;
Pred. No. 0.00e+00;
0; Mismatches 0
                      BP.
T 2
US-08-951-733-19 STANDARD; DNA; UNC; 3798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Oleski, Nancy A. RECISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-433B
TELECOMUNICATION INFORMATION:
TELEPHONE: (805) 447-6504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STRRET: One Amgen Center Drive
                                                                                          Sequence 19, Application US/08951733
Sequence 19, Application US/08951733
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (805) 499-8011
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 3798 base pairs
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Best Local Similarity 100.0%;
Matches 901; Conservative
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1909 GTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTA 1968
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OTHER INFORMATION: /Product= "human telomerase reverse OTHER INFORMATION: transcriptase (hTRT)"
SEQUENCE 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 901; DB 24; Length 4015;
Pred. No. 0.00e+00;
0; Mismatches 0; Indels 0
           COMPUTER READABLE FORM:
MEDIUM TYPE: RADABLE FORM:
MEDIUM TYPE: RADABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,919
FILING DATE: 31-MAR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 015389-003600US TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-0CT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-0CT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US U8/831,843
FRIDR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/914,549
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549
FRIOR DATE: 19-NOV-1997
FRIOR DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Parent, Annette S. REGISTRATION NUMBER: 42,058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4015 base pairs
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Best Local Similarity 100.0%;
Matches 901; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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   COUNTRY:
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2100 CTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTGCG 2159
                                                                                                                                                                                                          2280 GTACTGCGTCGGTCATATCCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGC 2339
                                                                                                                                                                                                                                                                                       2340 CITCAAGAGCCACGICICIACCITGAACAGACCICCAGCCGTACATGCGACAGIICGIGGC 2399
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APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Greeg B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and
TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGGGACGGCTCCTCCTGCTTTGGTGATTTCTTGTTGGTGACACCTCAC
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US-09-052-919-1 STANDARD; DNA; UNC; 4015 BP.
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California
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STATE:
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1909 GTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTA 1968
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transcriptase (hTRT) catalytic protein
component"
1363 C; 1275 G; 714 T; 0 OTHER.
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                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPBERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 05-MAY-1997
                                                                                               댠
                    APPLICANT: Morth, Gregg B.
APPLICANT: Morth, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Novel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                             PULGAZIA CALLON: 330
PRICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: APPIe. Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
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Pred. No. 0.00e+00;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /product- "htrt"
OTHER INFORMATION: /note- "human te.
OTHER INFORMATION: transcriptase (h:
OTHER INFORMATION: component"
SEQUENCE 4015 BP; 663 A; 1363 C; 1275 G;
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APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
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 Nakamura, Toru
Chapman, Karen
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LENGTH: 4015 base pairs
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Best Local Similarity 100.0%;
Matches 901; Conservative
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LOCATION: 56..3454
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            APPLICANT:
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          GTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTA 1979
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US-08-854-050-224 STANDARD; DNA; UNC; 4015
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Sequence 224, Application US/08854050
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
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Lingner, Joachim
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1920 GTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTA 1979
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Pred. No. 0.00e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
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REGISTRATION NUMBER: 015389-002600US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                             Two Embarcadero Center, 8th Floor San Francisco
THERAPEUTIC METHODS 335
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
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FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, RANGOLPH T.
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "hTRT"
                                                                                                                                                                                                                                                                                                    FILING DATE: 14-AUG-1997
LASSIFICATION: 435
LOR ADDITORNEY
LOR ADD
                                                                                                                                              United States of America
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Best Local Similarity 100.0%;
Matches 901; Conservative
TITLE OF INVENTION: THI
NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 56.3454
OTHER INFORMATION:
                                                                                                                         California
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                                                                ADDRESSEE:
                                                                                                                                            COUNTRY:
                                                                                STREET:
CITY: Se
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T: Lingner, Joachim
T: Nakamura, Toru
T: Chapman, Karen B.
T: Morin, Gregg B.
T: Harley, Calvin
T: Andrews, William H.
I: Andrews, William H.
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US-08-912-951-1 STANDARD; DNA; UNC; 4015
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Sequence 1, Application US/08912951
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
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                                                         COMPUTE: FALPY GISH
COMPUTE: FALPY GISH
COMPUTE: BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/09/026,981
FILING DATE: 20-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/064,322
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,762
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 60/054,549
FILING DATE: 01-AUG-1997
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Pred. No. 0.00e+00;
0; Mismatches 0.
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APPLICATION NUMBER: US 60/047,151
FILING DATE: 20-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                               Granahan, Patricia
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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1 Similarity 100.0%;
901; Conservative
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                                      COMPUTER READABLE FORM:
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              COUNTRY:
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                                                 CTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCG
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APPLICANT: Meyerson, Matthew
APPLICANT: Meyerson, Matthew
APPLICANT: Weinberg, Robert A.
ITILE OF INVENTION: Telomerase Catalytic Subunit Gene (NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Lew Militia Drive
CITY: Lexington
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       CTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGC
                 TCACCTGCAGGAGACCAGCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCT
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                                                                                GAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGT
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APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TILLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
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APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
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Sequence 1, Application US/08911312
GENERAL INFORMATION:
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LOCATION: 782..4177
COTHER INFORMATION: /Product= "human telomerase reverse OTHER INFORMATION: transcriptase (hTRT)"
OTHER INFORMATION: /Aote= "cDNA contained in plasmid OTHER INFORMATION: pGRN121"
SEQUENCE 7029 BP; 1416 A; 2122 C; 2051 G; 1440 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 901; DB 22; Length 7029; Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                           38,440
ER: 015389-002500US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                   FILING DATE: 18-APR-1997
PRIOR APPLICATION DATE:
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATE: 25-APR-1997
PRIOR APPLICATION DATE: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
                 APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/CDOCKET NUMBER: 0153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7029 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 100.0%;
Local Similarity 100.0%;
hes 901; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
PRIOR APPLICATION DATA:
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LOCATION: 1..4029
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                             NAME/KEY:
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                                              2580 CACGCTGCTGCAGCCTGTGCTACGCCACATGGAGAACAAGCTGTTTGCGGGGATTCG 2639
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                                                                                                                                           CACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCG 3354
                                                                       GAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGT
                                                                                                                                                                                                                CCACGCGAAAACCTICCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGT
                                                                                                                                                                                                                          2700 CCACGCGAAAACCTTCCTCAGGACCCTGGTCCCGAGGTGTCCCTGAGTATGGCTGCGTGGT
                                   TCACCTGCAGGAGCCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor
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US-08-854-050-173 STANDARD; DNA; UNC; 4029
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Novel Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States of America
                                                                                                                                                                                                                                                                                                                                                                 Sequence 173, Application US/08854050
Sequence 173, Application US/08854050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Two Embarcad
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1980 CGTCGTGGGGGGCCCAGAACGTTCCGCAGAAAAAAAAAGGGCCGAGCGTCTCACCTCGAGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /note= "preliminary sequence for OTHER INFORMATION: human TRT cDNA insert of OTHER INFORMATION: plasmid poRN121" SEQUENCE 4029 BP; 687 A; 1342 C; 1255 G; 720 T; 25 OTHER.
                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION PRIOR PRIOR APPLICATION FOR PRIOR APPLICATION PRIOR APPLICATION PRIOR PRIOR APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
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1904 GICCAGACICCGCTICAICCCCAAGCCIGACGGGCTGCGGCCGATIGTGAACAIGGACTA 1963
                                                                                                                                                                                                                                                                                                                                                                                              1920 GTCCAGACTCCGCTTCATCCCCAAGCCTGAGGGCTGCGGCCGATTGTGAACATGGACTA 1979
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                                                                                                                                                                                                                                           /note= "preliminary sequence for human TRT CDNA insert of plasmid pGRN121"
1342 C: 1255 G; 720 T; 25 OTHER.
                                                                                                                                                                                                                                                                                                            Score 898; DB 21; Length 40
Pred. No. 0.00e+00;
0; Mismatches 2; Indels
                                               REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
        ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                             99.7%;
Local Similarity 99.8%;
hes 899; Conservative
                                                                                                                                                                                                                             LOCATION: 1..4029
COTHER INFORMATION: /r
OTHER INFORMATION: hu
OTHER INFORMATION: pl
SEQUENCE 4029 BP; 687 A; 1:
 CLASSIFICATION: 536
                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                     FEATURE
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                                                               2760 GAACTTGCGGAAGACAGTGGTGAAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGC
                                                                                                                                                                                                                                           GCGGGACGGGCTGCTCCTGCGTTTGGTGATTTCTTGTTGGTGACACCTCACCTCAC
              GAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGT
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                                                                                                                                                                                                                                                                                    GAACTIGCGGAAGACAGTGGTGAACTICCCTGTAGAAGACGAGGCCCTGGGTGGCACGGC
                                                                                                                                                                                                                                CCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGT
                                                                                                                                                                                       #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 173, Application US/08651843
Sequence 173, Application US/08651843
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin
APPLICANT: Ancrews, William H.
TITLE OF INVENTION: Novel Telomerase
NUMBER OF SEQUENCES: 223
                                                                                                                                                                                                                                                                                                                                                                                                            7 9
US-08-851-843-173 STANDARD; DNA; UNC; 4029
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
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01-OCT-1996
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APPLICATION NUMBER: US 08
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
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APPLICATION NUMBER: U
FILING DATE: 01-OCT-1
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STATE: California
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2280 GIACTGCGTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGC 2339
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                                                                                                                                                                                                                                                                                          Score 508; DB 22; Length 2176;
Pred. No. 0.00e+00;
0; Mismatches 0; Indels 182; Gaps
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LOCATION: 1..2176
OTHER INFORMATION: /note- "clone 712562"
SEQUENCE 2176 BP; 432 A; 678 C; 642 G; 422 T; 2 OTHER.
NAME: Apple, Randolph T.
REGISSRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2176 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Local Similarity 79.8%;
hes 719; Conservative
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APPLICANT: Coch, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Angman, Karen B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND TITLE OF INVENTION: THERAPEUTIC METHODS
CORRESPONDENCE: 335
CORRESPONDENCE ADDRESS:
                                                                                                                                                       GAACTTGCGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGC 2803
                                                                                                                                                                     2760 GAACTTGCGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGC 2819
   2580 CACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCG 2639
                                                  GCGGGACGGGCTGCTCCTGCGTTTGGTGGATTTCTTGTTGGTGACACACCTCAC
                                                                                                             2700 CCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGT
                                 GCGGGACGGGCTGCTCCTGCGTTTGGTGATGATTTCTTGTTGGTGACACCTCACCTCAC
                                                                                              CCACGCGAAAACCTTCCTCAGGACCCTGGTCCCGAGGTGTCCCTGAGTATGGCTGCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 08/724,643
APPLICATION UNDER: US 08/724,643
APPLICATION 435
TITING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION: 435

APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION 3435
PRIOR APPLICATION A35
PRIOR APPLICATION UNMBER: US 08/844,419
FILING DATE: 18-APR-1997
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US-08-912-951-3 STANDARD; DNA; UNC; 2176
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CAPTURE READABLE FORM:
MEDIUM TYPE: Floppy disk
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Sequence 3, Application US/08912951
GENERAL INFORMATION:
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STATE: California
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                      CCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGT
                                                                                                                                                                                          and
                                                                                                                                       Sequence 36, Application US/09026981
Sequence 36, Application US/09026981
GENERAL INFORMATION:
APPLICANT: Counter, Christopher M.
APPLICANT: Weinberg, Robert A.
TITLE OF INVENTION: Telomerase Catalytic Subunit Gene NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; 965 G; 735 T; 2 OTHER.
                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/026,981
FILING DATE: 20-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                             STREE: Hamilton, Brook, Smith & Reynolds, STREE: Two Militia Drive CITY: Lexington
                                                                                                                       BP.
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REFERENCE/DOCKET NUMBER: WH197-11D4AM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
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US-09-026-981-36 STANDARD; DNA; UNC; 3346
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                 1920 GTCCAGACTCCGCTTCATCCCCAAGCCTGACGGCTGCGGCCGGTTGTGAACATGGACTA 1979
                                                                                             GTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTA 1310
                                    Gaps
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                                                 0; Indels 182;
    Length 3346;
Score 508; DB 23;
Pred. No. 0.00e+00;
                                                 0; Mismatches
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US-08-911-312-18 STANDARD; DNA; UNC; 3855
Similarity 79.8%;
19; Conservative
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2580 CACGCTGCTCTGCACCTGTGCTACCGCGACATGGACAAGCTGTTTGCGGGGATTCG 2639
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                                                                                                         2100 CICTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCCTCGTGCTGCTGCTGCGTGTGCG
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US-08-912-951-4 STANDARD; DNA; UNC; 3855 BP.
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                 APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Modrews, William
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.4%; Score 508; DB 22; Length 3855; 79.8%; Pred. No. 0.00e+00; Ative 0; Mismatches 0; Indels 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 56..2476
OTHER INFORMATION: /product= "hTRT"
OTHER INFORMATION: /note= "clone #712562"
SEQUENCE 3855 BP: 651 A; 1300 C; 1226 G; 678 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-40G-1997
CLASSIFICATION: 536
PRIOR APPLICATION UMBER: US 08/724,643
FILING APPLICATION NUMBER: US 08/724,643
FILING APPLICATION NUMBER: US 08/844,419
FILING APPLICATION NUMBER: US 08/844,419
FILING APPLICATION NUMBER: US 08/844,419
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICE TELEGRATION DATE:

PRIOR PAPLICATION NUMBER: US 08/854,050

PRIOR PAPLICATION DATA:

APPLICATION NUMBER: US 08/912,951

PRIOR PAPLICATION DATA:

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

ATONNEY/AGENT INFORMATION:

NAME: Enhorn, Gregory P.

REGISTRATION NUMBER: 38,440

RECISTRATION NUMBER: 38,440

RECISTRATION NUMBER: 38,400

RECISTRATION NUMBER: 38,760

TELEPHONE: (415) 576-0300

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGRAL SEG EN SEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Application US/08911312
Application US/08911312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Sequence 18, Applicati
Sequence 18, Applicati
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Sequence 4, Application US/08912951
Sequence 4, Application US/08912951
GENERAL INFORMATION:
CCEARD
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Gaps

Indels 182;

Conservative

Local Similarity nes 719; Conser

Best Loca Matches

2506

2566

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APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Adapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hariey, Calivin
APPLICANT: Hariey, Calivin
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "nucleic acid sequence with an open reading frame encoding a delta-18 variant polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: polypeptide"
SEQUENCE 3855 BP; 651 A; 1300 C; 1226 G; 678 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "delta-182 variant
                                                                                                                                                                                                                            ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 43.9

RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050

CLASSIFICATION 435

PRIOR APPLICATION 1435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843

CLASSIFICATION DATA:
APPLICATION UNMBER: US 08/846,017

FILING DATE: 25-APR-1997

CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

CLASSIFICATION 1435

PRIOR APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-CCT-1996

CLASSIFICATION NUMBER: 356,43

FILING DATE: 01-CCT-1996

CLASSIFICATION NUMBER: 015389-002600US

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3855 base pairs
                                                                                                                                                              LLP
                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                   COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 56.2479
OTHER INFORMATION: /
                                                                                                                                                                        STREET: Two Embarcad
CITY: San Francisco
STATE: California
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LOCATION: 1..3855
OTHER INFORMATION:
OTHER INFORMATION:
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GGCCCAGGACCGGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGTACGA 2208
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                                                 1920 GTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGACATGGACATA 1979
                                                                                       2520 GCGCATCAGGGGCAAGTCCTACGTCCAGGGGATCCCGCAGGGCTCCATCCTCT 2579
                                      1909 GTCCAGACTCCGCTTCATCCCCAAGCCTGAGGGTGCGGCTGCGGTTGTGAACATGGACTA 1968
                                                                             1969 CGTCGTGGGAGCCAGAACGTTCCGCAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGT 2028
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                                                                                                                   Length 3855;
Score 508; DB 22;
Pred. No. 0.00e+00;
                    0; Mismatches
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US-08-851-843-100 STANDARD; DNA; UNC; 2171
 Similarity 79.8%;
                   719; Conservative
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.9%; Score 477; DB 21; Length 2171; 79.6%; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 22..1716
OTHER INFORMATION: /note= "ECORI-NOtI insert of OTHER INFORMATION: clone 712562 encoding 63 kDa OTHER INFORMATION: telomerase protein" SEQUENCE 2171 BP; 433 A; 667 C; 641 G; 429 T; I OTHER.
                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843
FILING DATE: OG-MAY-1997
CLASSIFICATION: 536
                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                 APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Marann, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
APPLICANT: ANDREWS: 223
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            FILING DATE: 06-MAX-1997
CLASSIFICATION 536
PROR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
                                                                                                                                                                                      STATE: California
COUNTRY: United States of America
ZIP: 94111
                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
    Application US/08851843
Application US/08851843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01538
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 100:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2171 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 79.6%;
Matches 717; Conservative
Sequence 100, Applicati
Sequence 100, Applicati
GENERAL INFORMATION:
APPLICANT: Cech, Th
APPLICANT: Lingner,
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2100 CTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGCGCGC 2159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   888 GAACTIGCGGAAGACAGIGGIGAACTICCCIGIAGAAGACGAGGCCCIGGGIGGCACGGC 947
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351 GAAGGCACTGTTCAGCGTGCTCAACTACGAGCGGGCGCGGCGCCCCGGCCTCCTGGGCGC
                                                                                                                 CTCTGTGCTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCG
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                                                                                                                                                                                                                            471 GCCCCAGGACCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGTACGA
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US-08-854-050-100 STANDARD; DNA; UNC; 2171 BP
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APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
ITILE OF INVENTION: Novel Telomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 100, Application US/08854050
Sequence 100, Application US/08854050
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cech, Thomas R.
Lingner, Joachim
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2520 GCGCATCAGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCC 2579
2100 CTCTGTGCTGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCG 2159
                                                                                                                                                                                                                                                                                                                           2340 CTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGC 2399
                                                                                                                                                                                                                                                                                                                                                                                                           2400 TCACCTGCAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCT 2459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2460 GAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGT 2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       666 ------CTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTC
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                                          471 GCCCCAGGACCCGCCCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCCGCGTACGA
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                                                                                                                                                                                                                                                                                     650 CTTCAAGAGCCACGTC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 22..1716

OTHER INFORMATION: //note= "ECORI-Not1 insert of OTHER INFORMATION: clone 712562 encoding 63 kDa OTHER INFORMATION: telomerase protein" SEQUENCE 2171 BP; 433 A; 667 C; 641 G; 429 T; 1 OTHER.
                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 52.9%; Score 477; DB 21; Best Local Similarity 79.6%; Pred. No. 0.00e+00; Matches 717; Conservative 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      015389-002930US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: U1-OCT-1996
CLASSIFICATION: 536
ATTONENY/AGENT INFORMATION:
NAME: APPLE, Randolph T.
REGISTRATION NUMBER: 36,429
RESINCE/DOCKET NUMBER: 015389-002
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
FUNCTH: 2171 base pairs
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/854,050 FILING DATE: 09-MAY-1997 CLASSIFICATION: 536
                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

 $\mbox{n.a.}$  -  $\mbox{n.a.}$  -  $\mbox{n.a.}$  database search, using Smith-Waterman algorithm with gap extension penalties as well as gap opening penalties MPsrch_nna

Thu Dec 24 18:29:00 1998; MasPar time 74.84 Seconds 561.595 Million cell updates/sec Run on:

Tabular output not generated.

Title:

>US-08-951-733-13
(1920-2820) from USO8951733.seq (2 of 2)
901
1920 GTCCAGACTCCGCTTCATCC......AGGCCCTGGGTGGCACGGCT 2820
CAGGTCTGAGGCGAAGTAGG......TCCGGGACCCACGTGCGCGA Description: Perfect Score: N.A. Sequence:

Scoring table:

TABLE default Gap open 30; Gap extend 1

Dbase 0; Query 0 Nmatch STD 88822 seqs, 23323279 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

n-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 8.416; Variance 4.601; scale 1.829

Statistics:

## SUMMARIES

Š.	Score	Match	Match Length DB	BB	ID	Description	Pred. No.
1	39	4.3	7218	-	US-08-232-	Sequence 14, Applicati	4.38e-11
7	30	3.3	215	-	US-08-238-	Sequence 5, Applicatio	1.52e-05
e U	28	3.1	215	ч	US-08-238-	'n	7
4	26	2.9	74	~	PCT-US95-1	Sequence 94, Applicat	m ·
ß	26	2.9	81	7	PCT-US95-1	Sequence 92, Applicati	3.08e-03
9	25	7.8	74	7	PCT-US95-1	Sequence 100, Applicat	1.11e-02
7	25	2.8	75	~	PCT-US95-1	Sequence 99, Applicat:	1.11e-02
œ د	25	2.8	81	7	PCT-US95-1	Sequence 98, Applicati	1.11e-02
<u>ი</u>	25	2.8	81	7	PCT-US95-1	Sequence 92, Applicati	1.11e-02
10	25	2.8	82	7	PCT-US95-1	97,	1.11e-02
11	25	2.8	7218	٦	US-08-232-	Sequence 14, Applicati	1.11e-02
12	24	2.7	74	~	PCT-US95-1	Sequence 100, Applicat	3.90e-02
c 13	24	2.7	74	~	PCT-US95-1	94, 2	3.90e-02
c 14	24	2.7	75	7	PCT-US95-1	Sequence 99, Applicati	3.90e-02
15	24	2.7	81	7	PCT-US95-1	Sequence 98, Applicat	3.90e-02
19	24	2.7	82	~	PCT-US95-1	Sequence 97, Applicati	3.90e-02
17	23	5.6	99	-	US-08-471-	Sequence 144, Applicat	1.34e-01
c 18	23	5.6	99	٦	US-08-471-	Sequence 144, Applicat	1.34e-01
19	23	5.6	69	~	US-08-471-	Sequence 142, Applicat	1.346-01

1.34e-01 1.34e-01 1.34e-01 1.34e-01 1.34e-01 1.34e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-01 4.51e-
Sequence 142, Applications Sequence 120, Applications Sequence 25, Applications Sequence 25, Applications Sequence 25, Applications Sequence 143, Applications Sequence 143, Applications Sequence 143, Applications Sequence 1, Applications Sequence 143, Applications Sequence 1, Application
US-08-471- US-08-209 US-08-133- US-08-133- US-08-471- US-08-471- US-08-471- US-08-471- US-08-456- US-08-456- US-08-456- US-08-457- US-08-457- US-08-457- US-08-457- US-08-457- US-08-457- US-08-457- US-08-457- US-08-457- US-08-457- US-08-457- US-08-457- US-08-457- US-08-471- US-08-471- US-08-471- US-08-471- US-08-273- US-08-273- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-07-745- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-471- US-08-47
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## ALIGNMENTS

STATE: ALEXAUGITA
STATE: VA
COUNTRY: USA
ZIJ19-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC-DS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE: CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
ATORNEY/AGENT INPORMATION:
NAME: BENT, Stephen A
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
RECOMMUNICATION NUMBER: 29,768
RECOMMUNICATION NUMBER: 29,768
RECOMMUNICATION NUMBER: 29,768
RECOMMUNICATION NUMBER: 29,768
RECERRICE/DOCKET NUMBER: 29,768
RECERRICE/DOCKET NUMBER: 29,768
RECERRICE/DOCKET NUMBER: 29,768
RECERRICE/OMOUNICATION NUMBER: 29,768
RELEPHON: (703)836-9300
TELEFRAX: (703)836-9300 Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
GENERAL INFORMATION:
APPLICANT: DORNER, F. APPLICANT: SCHETFLINGER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: ADDRESSE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500
CITY: Abexandria US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP TELEX: 899149 INFORMATION FOR SEQ ID NO: 14: XXXXXX RESULT 

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APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, John M.
APPLICANT: POWELL, An
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MINVIMSSSSVVSRIASCNDKAKKDGNITSSWTTDCCNRTWGVCDTDTIYRVNNDSGHNK 60
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INPORMATION: /Standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 GACCCGCCCGCCTGAGCTTTGTCAAGGTGGATGTGACGGCGCG 2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YSSANYNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNG 108
                                                                                                                                                                                                                                                                                                                                                                              Match 3.3%; Score 30; DB 1; Length 215; Local Similarity 14.8%; Pred. No. 1.52e-05; es 16; Conservative 46; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
US/08/238,163
FILING DATE: 03-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JT 3
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
                  NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
GENERAL INFORMATION:
                                                                                   TELEPHONE: (415) 543-5600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDENNESS: single
   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                   TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 0. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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APPLICANT: BENNETT, Alan
APPLICANT: DOWELL, Ann
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                   2354 TCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGA 2413
                                                                                                                                                                                                                                                                                                          2474 GIGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACCACGCGCGATCAGGGGCA 2533
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2534 AGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGCTCCATCCTCCTCCTCCTGCTCTGCA 2593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2594 GCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGGATTCGGCGGGACGGCTGC 2653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2654 TCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCCTCACCCCACGCGAAAACCT, 2713
                                                                                                                                                                                                  ô
                                                                                                     CLONE: PTZ9Pt-FIS
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                                           Query Match 4.3%; Score 39; DB 1; Length 7218; Best Local Similarity 1.1%; Pred. No. 4.38e-11; Matches 4; Conservative 201; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JT 2
US-08-238-163-5 STANDARD; DNA; UNC; 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
*CLASSIFICATION: 800
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1429 YYYYYGTACC 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::::: | |||
2714 TCCTCAGGACC 2724
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STATE: New COUNTRY: US ZIP: 10036
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                                                                                                                                                                                                                  95 TDSYNASGISSSNGGTDGNRSGADSYGSSKTAMTSRNRTGKTANNAVDSRNMGDASVGSD 154
                                                                                                                                                                          35 DCCNRTWGVCDTDTTYRVNNDSGHNKYSSANYNYGGNNVGAAKTHYYTHTNVSGADSKTV 94
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                   Sequence 94, Application PC/TUS9511934
Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICART: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                        ö
                                                                   NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: /Standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP: 15 A: 8 C: 25 G: 26 T: 141 OTHER.
                                                                                                                                                                                                                                                                         155 KNTKKHAKNSADGKVGSKNNGDRNNRYGTGTKSNVSNNCGGGNKRDVSSY 204
                                                                                                                                 Score 28; DB 1; Length 215;
Pred. No. 2.24e-04;
62; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 96990
TELEX: 66141 PENINE
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
                                                                                                                                                                                                                                                                                                             T 4
PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
       LENGTH: 215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS
                                                                                                                                 3.1%;
Local Similarity 14.1%;
les 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                      TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                Sequence 92, Application PC/TUS9511934
Sequence 92, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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  Score 26; DB 2; Length 74; Pred. No. 3.08e-03; 19; Mismatches 43; Indels
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Pred. No. 3.08e-03;
19; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION NATH: PCT/US95/11934
FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 6
PCT-US95-11934-100 STANDARD; DNA; UNC; 74 BP.
                                                                                                                                                                                                                                                                     1101-196-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 92:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.9%;
Best Local Similarity 11.4%;
Matches 8; Conservative
Query Match
Best Local Similarity 11.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                          : : ||||||
2508 CCACCACGCC 2517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2508 ccaccaccc 2517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                63 BNNBNACGCC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 BNNBNACGCC 79
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US-08-951-733-13-03.rni

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Sequence 98, Application PC/TUS9511934
Sequence 98, Application PC/TUS9511934
Sequence 98, Application PC/TUS9511934
Sequence 98, Application PC/TUS9511934
SEREAL INFORMATION:
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTY: New York
COUNTY: New York
STATE: New York
COUNTYER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION NUMBER: PCT/US95/11934
FILING DATE: XNORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 25; DB 2; Length 75;
Pred. No. 1.11e-02;
20; Mismatches 42; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 75 BP: 1 A; 1 C; 7 G; 5 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .r 8
PCT-US95-11934-98 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
RELECOMMUNICATION: INFORMATION:
TELECHONNE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                      1101-196-228
                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFX: (512) 869-9741/8864
INFORMATION FOR SEG ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.8%;
Best Local Similarity 8.8%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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1981 GTCGTGGG 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NNBNNBGG 68
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   GENERAL INFORMATION:

APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CTTY: New York
COUNTY: USA
ZIP: New York
COUNTY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSITICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSITICATION NUMBER: 18,872
CLASSITICATION NUMBER: 18,872
REGISTATION NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEFRANE (212) 869-9741/8864
TELEFRAX: (6141 PENIE
INFORMATION FOR SED ID NO: 100:
SEQUENCE CHARACTERISTICS:
LEBOTH: 74 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 99, Application PC/TUS9511934

C GENERAL INFORMATION:
C APPLICANT: Cytogen Corporation
C TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
C CORRESPONDENCE ADDRESS:
C ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
C CIT: New York
C CITY: New York
C COUNTRY: USA
C ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Natch 2.8%; Score 25; DB 2; Length 74; Local Similarity 10.1%; Pred. No. 1.11e-02; Pred. 7; Conservative 20; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 7
PCT-US95-11934-99 STANDARD; DNA; UNC; 75 BP.
                                 Sequence 100, Application PC/TUS9511934 Sequence 100, Application PC/TUS9511934 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2299 CATACCGAC 2291
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Best Loca Matches

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0; Gaps

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2617 TCTCCATGTCGCCGTAGCACAGGCTGCAGCGTGGAGGAGGATGGAGCCCTGCGGGA 2558
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Sequence 97, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25; DB 2; Length 82;
Pred. No. 1.11e-02;
20; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CANRENT APPLICATION DATA:
CAPPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
SEQUENCE 82 BP; 1 A; 2 C; 10 G; 8 T; 61 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JI 11
US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
                                                                                             T 10
PCT-US95-11934-97 STANDARD; DNA; UNC; 82 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1101-196-228
                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18 872
REFERRNCE/DOCKET NUMBER: 1101-1
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08232463 Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.8%;
Best Local Similarity 8.8%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DORNER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                            CITY: New York STATE: New York
                                                  2557 TCCCCTGGCAC 2547
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                            66 NBNNBNNBNAC 76
                                                                                                                                                                                                                                                                                                                       USA
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CC CC
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                                                                                                                                                                                                              2359 TAGAGACGTGCTCTTGAGGCCTTGCGGACGTGCCCATGGGCGGCCTTCTGGACCACGG 2300
                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                        Sequence 92, Application PC/TUS9511934
Sequence 92, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
                                                                                                                                      Score 25; DB 2; Length 81;
Pred. No. 1.11e-02;
20; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.8%; Score 25; DB 2; Length 81; 9.9%; Pred. No. 1.11e-02; ative 20; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18, 20, 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
SEQUENCE 81 BP: 3 A: 5 C; 6 G; 4 T; 63 OTHER.
                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 81 BP; 6 A; 6 C; 4 G; 5 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                                    JT 9
PCT-US95-11934-92 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 790-9090
TELERA: (212) 869-9741/8864
TELER: (614) PENNIE
INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 11-
TELECOMMUNICATION INFORMATION:
              98:
          INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                      Query Match 2.8%;
Best Local Similarity 10.1%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 9.9%;
Matches 7; Conservative
66141 PENNIE
                                                                                                                                                                                                                                                                            2299 CATACCGAC 2291
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TELEX:
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Gaps

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2268 ACCCCA 2273
                                   COUNTRY: UZIP: 10036
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  2079 CCGCGCCCCGCTCGAGTAGAGCACGCTGAACAGTGCCTTCACCCTCCAGGTGAGACGCTC 2020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 100, Application PC/TUS9511934
Sequence 100, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: pTZgpt-F1s
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 1; Length 7218;
Pred. No. 1.11e-02;
76; Mismatches 53; Indels
                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
     APPLICANT: FALKNER. F. G.
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       APPLICALL...

FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313

FILING DATE: 26-AUG-1991
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
CTELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
""TELEPHONE: (703)836-9300
""TELEPHONE: (703)683-4109
                                                                                                                                                                                                                                                                                                                      30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 12
PCT-US95-11934-100 STANDARD; DNA; UNC; 74 BP.
                                                   ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CIIY: Alexandria
                                                                                                                                                                                                                                                                                                                                                  TELERAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.8%;
Best Local Similarity 1.5%;
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                       STATE: VA
COUNTRY: USA
ZIP: 22313-0299
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1959 CCGCAGCCCGT 1949
                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: line
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2208 GGGCGCGTACGACCATCCCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAA 2267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 94, Application PC/TUS9511934
Sequence 94, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 2.7%; Score 24; DB 2; Length 74; Best Local Similarity 7.6%; Pred. No. 3.90e-02; Matches 5; Conservative 20; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
                                                                                                                                                                Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JT 13
PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
                                                                                                                                                                                                                                                                                                                    1101-196-228
                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-22
FIELECOMUNICATION INFORMATION:
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTE: New York
COUNTER: USA
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US95/11934 FILING DATE: 20-SEP-1995 CLASSIFICATION: ATTORNEY AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION
TELEPRONE: (212) 790-9090
TELERA: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                 New York
: New York
RY: USA
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XXXXXX
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                                                                                                                                                                 2274 CTGGGGTTTGATGTGGTGGCGATGACCTCCGTGAGCCTGTCGGGGATGGTGTGTA 2215
                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 99, Application PC/TUS9511934
Sequence 99, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
TITLE OF INVENTION: Peptide Libraries
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA

ZIP: 10036
COMPUTER TADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
APPLICATION NUMBER: 10-196-228
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEFAX: (217) 80-9090
TELEFAX: (217) 869-9741/8864
TELEFX: 614 PENNIE
LENGTH: 75 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
C TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                     Score 24; DB 2; Length 74;
Pred. No. 3.90e-02;
20; Mismatches 39; Indels
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 869-9741/8864
TELEFAX: (614) PENNIE
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENNESS: SINGLE
                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
                                                                                                                                                                                                                                                                                                                                                 л 14
РСТ-US95-11934-99 STANDARD; DNA; UNC; 75 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                     Query Match 2.7%;
Best Local Similarity 6.3%;
Matches 4; Conservative
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DB 2; Length 75;

2.7%; Score 24;

Query Match

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                         0; Gaps . 0;
                                                                                                                   2624 AGCTIGIICICCAIGICGCCGIAGCACAGGCIGCAGAGCAGCGIGGAGGAIGGAGCC 2565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 98, Application PC/TUS9511934

C Sequence 98, Application PC/TUS9511934

C SENERAL INFORMATION:
C APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Peptide Libraries
C NUMBER OF SEQUENCES: 103
C CORRESPONDENCE ADDRESS:
C STREET: 1155 Avenue of the Americas
C CITY: New York
C COUNTRY: USA
C COUNTRY: USA
C CITY: New York
C COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 2.7%; Score 24; DB 2; Length 81; Best Local Similarity 7.6%; Pred. No. 3.90e-02; Matches 5; Conservative 20; Mismatches 41; Indels
Pred. No. 3.90e-02;
20; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
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SEQUENCE 81 BP; 6 A; 6 C; 4 G; 5 T; 60 OTHER.
                                                                                                                                                                                                                                                                                                LT 15
PCT-US95-11934-98 STANDARD; DNA; UNC; 81 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: Thu Dec 24 18:30:36 1998 Job time: 96 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 790-9090
TELERA: (212) 869-9741/8864
TELERA: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
Best Local Similarity 6.2%;
Matches 4; Conservative
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TOPOLOGY: lir
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2564 TGCGG 2560
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C C C C C C C C C C C C C C C C C C C	0000 0000	0 4444 45 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT LOCUS DEFINITION	ACCESSION NID KEYWORDS SOURCE ORGANISM	REFERENCE	TITLE JOORNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOURCE SOURCE GOVERNMENT
	MPsrch_nna n.a n.a. database search, using Smith-Waterman algorithm with gap extension penalties as well as gap opening penalties Run on: Thu Dec 24 19:23:48 1998; MasPar time 12290.10 Seconds Tabular output not generated.  Title: Description: (1-3798) from US08951733.seq Perfect Score: 3798 N.A. Sequence: GGTGCGCAGGCCCGTCGCGAACGCTGGAATAGTCCATCCCTGAT 3798 Comp.	Scoring table: TABLE default Gap open 30; Gap extend 1 Nmatch STD: Dbase 0; Query 0 Searched: 567134 seqs, 1101898692 bases x 2	ocessing:	Database: embl55 Inch 2 :em_fun 3:em_htg 4:em_huml 5:em_hum2 6:em_in 7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_p1 13:em_ro 14:em_vi Database: genbank107 15:gb_baal 16:gb_ba2 17:gb_htg 18:gb_in 19:gb_om 20:gb_ov 21:gb_pat 22:gb_ph 23:gb_pl1 24:gb_pl2 25:gb_pr1 26:gb_pr2 27:gb_pr3 28:gb_ro 29:gb_st 30:gb_sy 32:gb_un 33:gb_vi	Statistics: Mean 11.964; Variance 6.048; scale 1.978	o. is the number of results predicted by chance to have a reater than or equal to the score of the result being printe derived by analysis of the total score distribution.  SUMMARIES  Query	1079 1079 1079 1079 1079 1079 1079 1079

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4015 bp mRNA PRI 16-AUG-1997 telomerase reverse transcriptase (hTRT) mRNA, complete
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  (24-JUL-1997) Geron Corporation, 230 Constitution Drive,
k, CA 94025, USA
Location/Qualifiers
    5.30e-02
5.330e-02
5.330e-02
5.330e-02
1.81e-01
1.81e-01
1.51e-03
1.96e+00
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a; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T.M., Morin,G.B., Chapman,K.B., Weinrich,S.L.,
H.H., Lingner,J., Harley,C.B. and Cech,T.R.
e catalytic subunit homologs from fission yeast and 177 (5328), 955-959 (1997)
Synthetic DNA for prep S.griseus gene for prep DNA encoding envelope Epstein-Barr virus (WI Methylobacterium extor Human DNA sequence fro *** SEQUENCING IN PROG HOMO sapiens DNA polymer Mustela vison microsat S.marcescens proBA gen Drosophila melanogaste Epstein-Barr virus (B9 S.coelicolor 6 actyA r Azotobacter vinelandii S.pombe chromosome I C Human DNA sequence fro Drosophila melanogaste Drosophila melanogaste Drosophila melanogaste Human DNA sequence fro Drosophila melanogaste Human DNA sequence *** Epstein-Barr virus (EB Epstein-Barr virus, ar Homo sapiens Shox gene *** Epstein-Barr virus, ar Homo sapiens Chromosom
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Matches 3785; Conservative
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	1981   CAGAACGTTCCGCAGAGAAAGAGGGCCGAGCGTCACCTCGAGGGTGAAGGCACTGTT		2281 2293 2341 2353 2401	2413 GACCAGCCCGC 2461 CAGTGGCCTCT 2473 CAGTGGCCTCT 2521 CAAGTCCTACC 11111111111111111111111111111111	11111111111111111111111111111111111111	2761 GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGGCTTTTGTTCAGAT 2820
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mRNA PRI 29-AUG-1997 ise catalytic subunit (hEST2) mRNA, complete 2940 2952 AGGICAACAGCCICCAGACGGIGIGCACCAACAICIA 3060 ACAGGITICACGCAIGIGCIGCAGCICCCAIIICA 3120 CATTITICCTGCGCGTCATCTCTGACACGGCCTCCCT 3180 AGAACGCAGGGATGTCGCTGGGGGCCAAGGGCCCCGC 3240 ### STATE STATES AND A STATES A 3420 3480 SGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTG 3600 STCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT 3660 ITTCACTICCCCACAGGCIGGCGCTCGGCTCCACCCCA 3720 GCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780 GGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGT 2892 CCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG TCCTGGACTGATGGCCACCGCCCACAGCCAGGCCGA CGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGC

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PGARRRGGSRSLPLPRRRGAAPEPERTPVGGSWAHPGRTRGFBGRGFCVVSPA
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LLRGHSSPWQVYGFVRACLRRLVPPGLUMGSRHNBRRFLRNTKRFISLGGEL
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GGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRR
KLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQVWKNPT
                                                                                                                Meyerson, M., Counter, C.M., Eaton, E.N., Ellisen, L.W., Steiner, P., Caddle, S.D., Zlaugra, L., Beljersbergen, R.L., Davidoff, M.J., Liu, Q., Bacchetti, S., Haber, D.A. and Weinberg, R.A. hEST2, the putative human telomerase catalytic subunit gene, is up-regulated in tumor cells and during immortalization (2011) 90 (4), 785-795 (1997)
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YVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD"
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                                                 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Meyerson,M., Counter,C.M., Eaton,E.N., Ellisen,L.W., Steiner,P.,
Gaddle,S.D., Zaugra,L., Beijersbergen,R.L., Davidoff,M.J., Liu,
Caddle,S.D., Zaugra,L., and Welnberg,R.A.
Direct Submission
Submitted (11-AUG-1997) Whitehead Institute for Biomedical
Research, Massachusetts Institute of Technology, Nine Cambridge
Center, Cambridge, MA 02142, USA
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product="telomerase catalytic subunit"
/db_xref="PID:3023055"
/translation="MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            see GenBank Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            artificial sequence.

1 (bases 1 to 8960)

2 (conter,C.M., Meyerson,M., Eaton,E.N., Ellisen,L.W., Caddle,S.D.,
Haber,D.A. and Weinberg,R.A.
Telomerase activity is restored in human cells by ectopic
expression of hTRRT (hEST2), the catalytic subunit of telomerase on the sequence of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic construct human telomerase catalytic subunit (hTERT/hEST2) mRNA and 3' Influenza A hemagglutinin tag, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Counter, C.M., Meyerson, M., Eaton, E.N., Ellisen, L.W., Caddle, S.D. Counter, C.M., Meyerson, M., Eaton, E.N., Ellisen, L.W., Caddle, S.D. Counter, C.M., Meinberg, R.A.

Birect Submission
Submission
Submitted (20-7AN-1998) Whitehead Institute, 9 Cambridge Center, Cambridge, MA 02142, USA
Location/Qualifiers
1. .8960
                                                                                                                                                                             3562
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                                                                                                                     3551
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/db_xref="taxon:4572"
1102. .4542
/note="telomerase catalytic subunit hTERT/hEST2 mRNA"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3743 TICCTCACCAGGAGCCCGGCTICCACTCCCCACATAGGAATAGTCCATCCCTGAT 3798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3732 IICCICACCAGGAGCCCGGCIICCACICCCCACAIAGGAAIAGICCAICCCCAGAI 3787
3563 CCCGCACCGCTGGGAGTCTGAGGCCTGAGTGTTTGGCCGAGGCCTGCATGTCCGGC
                                                             3443 GACTICAAGACCAICCIGGACIGAIGGCCACCCGCCCACAGCCAGGCCGAGAGCAGACAC
                                                                                                                                                                                                                                              CCCGCACCGCTGGGAGTCTGAGGCCTGAGTGTTTTGGCCGAGGCCTGCATGTCCGGC
                                                                                                                                                                                                                                                                                                                                                                 TGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAG
                                                                                                                     1147. .4605
/note="telomerase/reverse transcriptase"
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/db_xref="taxon:32630"
order[1..1101,4606..8960)
/note="mammalian expression vector;
Number U47120"
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1147. .4605
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1102, .454;
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/note="engineered based on the epitope for the anti-influenza virus hemagglutinin monoclonal antibody 12C45; similar to part of the Influenza A hemaglutinin gene sequence in GenBank Accession Number M29257"
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Pred. No. 0.00e+00;
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	GAAGGCGTCTG	GAAGGCGTCTG	TGGGCCTGCCA	TGGGCCTGCCA	TGCCCAAGAGG	TGCCCAAGAGG	GGTCCTGGGCC	GGTCCTGGGCC	CACCTGCCAGA	CACCTGCCAGA	ACTCCCACCCA	ACTCCCACCCA	CACGTCCCTGG	CACGICCCIGG	CCTCAGGCGAC	CCTCAGGCGAC	TGACTGGCGCT	TGACTGGCGCT	GGACTCCCCGC	GGACTCCCCGC	TGGAGCTGCTT	TechecTecTT	CGCTGCGAGCT	CGCTGCGAGCT		CTGTGGCGGCC	AGCACAGCAGC	AGCACAGCAGC					16166667767 	ACCGTCTGCGT	ACCGTCTGCGT(	,
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3861 GAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCA 3920 CTTCGACGTCTTCCTACGCTTCATGTGCCACCACCGCCGTGCGCATCAGGGCCAAGTCCTA 3081 CCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCT 2002 CCGCAGAGAAAAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCT TAICCACAGGGCCTGGCGCACCTTCGTGCTGCGGGCCCCAGGACCCGGCCGCCTGA CGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCCACGCTGCTGCAGCCTGTG AAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGA CAAGCCTGAGGGCCGGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTT GCTGAGGGATGCCGTCGTCATCGAGCAGGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCT CTACGGCGACATGGAGAACAAGCTGTTTGCGGGGGATTCGGCGGGGACGGGCTGCTGCG GACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGAACTTGCGGAAGACAGTGGT GGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCC 

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VOGELRACICK VVOASLOFTRHURERFEKNIKK FEIGLGKYGKLSLOELAWRKINCEDCH
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RKSWRSKLOSIG VROHLERVRIKEELSGGEFHHOOTWAMP TOKREF FEK PROHGLRFIV
NSSYSMGTRALGRRKQAOHTTORIKTLESMLNYERTKHPHLMGSSVLGMND ITRTWRA
DSQCQVHKSFRROYTLSDLOPYROGFIKHLDSDAARNRSVIT ROGISLANDESSSIL
FOBFLHFIRHSVNT IGDGYTOCOLPOGSSISTLLCSICFODMENKLFSEVORDGLL
LRRVDDFLLVTPHLDOAKTELSTLUGGSSSISTLLCSICFODMENKLESVUR
LRRVDDFLLVTPHLDOAKTELSTLUGGSSISTLLCSICFODMENKLESVUR
LKCHGLFLDLOVNSLOTVTCSISTRACITLOSICKRAGKTMRNKLLSVLR
LKCHGLFLDLOVNSLOTVTILKSSTRAGTILLGAY FFHACVIQLPPORVRNILTFFLGIIS
SQASCCYALIKVNROGMTLARAGSFPPBAAHNLCYQAPLLKLAAHSVIYKCLLGPLRT
SQASCCYALIKVNROGMTLARAGSFPPBAAHNLCYQAPLLKLAAHSVIYKCLLGPLRT
SQASCCYALIKVNROGMTLARAGSFPPBAAHNLCYQAPLLKLAAHSVIYKCLLGPLRT
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KIYRTLVAQCLVCMHWGSQPPPADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFE
                                                                                                                            LLNBARGGPPMAFTSSVRSYLPNTVIETLRVSGAMMLLLSRVGDDLLVYLLAHCALYL
LVPPSCAYQVGGSPLYQICATTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQE
APXPLALPSRGTKRHLSLTSTSVPSAKKARCYPVPRVEEGPHRQVLPTPSGKSWVPSP
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                        /codon_start=1
/product="telomerase catalytic subunit"
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Pred. No. 0.00e+00;
0; Mismatches 988;
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Martin-Rivera, L., Herrera, E. and Blasco, M.A.
Direct Submission
Submitted (19-JUN-1998) Immunology and Oncology, National Centre Biotechnology, Cantoblanco, Madrid 28049, Spain
Location/Qualifiers
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3369)
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Expression of mouse telomerase catalytic subunit in embryos
adult tissues
Proc. Natl. Acad. Sci. U.S.A. 95 (18), 10471-10476 (1998)
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1 (bases 1 to 3426)
Greenberg,R.A., Allsopp,R.C., Chin,L., Morin,G.B. and Depinho,R.A.
Expression of mouse telomerase reverse transcriptase during development, differentiation, and proliferation
Chocogene (1998) In press
Chases 1 to 3426)
Chases 1 to 3426
Chemberg,R.A., Allsopp,R.C., Chin,L., Morin,G.B. and Depinho,R.A.
Direct Submission
Submitted (02-MAR-1998) Microbiology and Immunology, Albert
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Einstein College of Medicine, 1300 Morris Park Ave., Bronx,
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Uppublished
2 (bases 1 to 201)
Drissi,R. and Cleveland,J.L.
Direct Submission
Submitted (07-ocr-1997) Biochemistry, St jude Children's Research
Hospital, 332 North Leuderdale, Memphis, TN 38105, USA
Location/Qualifiers
3076 GATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCA 3135
                                                                                                                                                                                                                                                              | GCGTGTTAGGAAGAACCTCACATTCTTTCTGGGCATCATCTCCAGCCAAGCATCCTGCTG 3136
                                                                                                                                                                                                                                                                                                                                                                    ----TTCCTCCTGAAGCCGCACATTGGCTCTGCTACCAGGCCTTCCTGCTCAAGCTGGC 3247
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                                                                                                        CTTCAAAGCTGGGAAGACCATGCGGAACAAGCTCCTGTCGGTCTTGCGGTTGAAGTGTCA 2956
                                                                                                                                                         GATCTTCCTGCTTCAGGCCTACAGGTTCCATGCATGTGTGATTCAGCTTCCCTTTGACCA 3076
                                                                                                                                                                                                                                                                                       GCAAGITIGGAAGAACCCCACAITITICCIGCGCGTCAICTCTGACACGGCCICCCTCIG 3195
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1 (bases 1 to 201)
Drissi, R. and Cleveland, J.L.
Partial sequence of Mus musculus telomerase catalytic subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF029235 201 bp mRNA ROD 12-NOV-1997
Mus musculus telomerase catalytic subunit mRNA, partial cds.
AF029235
                                                     CTGTGACTACTCAGGTTATGCCCAGACCTCAATTAAGACGAGCCTCACCTTCCAGAGTGT
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/product="telomerase catalytic subunit"
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/organism="Mus musculus"
/db_xref="taxon:10090"
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/db_xref="PID:g2605903"
/translation="PFYVTESTFQKNRLFFYRKSVWSKLQSIGVRQHLERVRLRELSQ
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                                                                                                          Length 201;
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Similarity 2.4%; Pred. No. 5.33e-26;
9; Conservative 211; Mismatches 153; Indels
                                                                                                       Score 129; DB 28; Length 20
Pred. No. 7.48e-73;
0; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 7218)
Dorner,F., Schefflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23 SEP-1997;
Location/Qualifiers
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Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Davis, C.A., Kadner, K., Miguel, T., Pitluck, S., Pollard, M., Cheng, J., Subramanian, S. and Martin, C.H.
Rojeski, H., Subramanian, S. and Martin, C.H.
Boirect Submission
Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A.
Sequence submitted by:
DOE Joint Genome Institute.
Location/Qualifiers
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/standard_name="RLF"
/note="65% & 69% protein identity GenPept:U22377"
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228. gs503
rrpt_family="Alu"
070. 9387
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                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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/rpt_family="Alu"
13727. 13750
/note='(AC)12"
/rpt_type=tandem
/rpt_unit=AC
13783. 14024
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/rpt_family="Alu"
2295. .2438
/rpt_family="Alu"
2818. .2859
/note="(GT)21"
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/rpt_family="Alu"

527..5602

/rpt_family="Alu"

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/rpt_family="LI"
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3707. .3728
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14175. 14470
/rpt_family="Alu"
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2057. .12085
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/rpt_unit=CA
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/chromosome="5"
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'note="(CA)19"
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/note="(A)22"
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12365. .1264
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Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete
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Ricke.D.O.
Comparison Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
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1 (bases 1 to 74371)

Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Kadner,K., Miguel,T., Miller,C., Pilluck,S., Pollard,M., Rojeski,H., Subramanian,S. and Martin,C.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.3%; Score 49; DB 21; Length 721
Best Local Similarity 2.0%; Pred. No. 1.39e-13;
Matches 6; Conservative 165; Mismatches 122; Indels
                                                                                                                                                                                                                                                         Dorner, F., Scheiflinger, F. and Falkner, F. Gunter. Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
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                                                                                                                               Sequence 14 from patent US 5670367.
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92724471
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Unclassified.
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join(28485. .29559, 29598. .29779)
foin(28485. .29559, 29559. .39779)
force="958 identity dbsTs:G14522 (SHGC-11312)"
894955. .29976
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/note="GRAIL 2 excellent exon, frame 1"
complement(32159. .32232)
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/rpt_unit=A
28712. 28930
/rpt_family="MER20"
complement(28769. 28838)
/note="GRALL 2 excellent exon, frame
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// Standard_name="A1027942"
// note="100% identity EST ov84a10.x1"
// complement(30401. .30536)
// note="GRAIL 2 excellent exon, frame /rpt_family="MIR"
'standard_name="possible repeat"
.5300. .15613
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3022. .23326
                                                                                                        complement(16675, .16977)
/rpt_family="Alu"
complement(16993, .17085)
/rpt_family="MER42"
complement(1789, .18276)
/rpt_family="Alu"
19305, .19583
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/rpt_family="MER42"
complement(25349. .25713)
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complement(25727. .26471)
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23744. .23767
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28040. .28066
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22017. .22038
/note="(A)22"
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16671. .16690
/note="(T)20"
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Complement(34021. 34144)

/note="GRALL 2 excellent exon, frame 2"

complement(35238. 35331)

/note="GRALL 2 excellent exon, frame 1"

/note="GRALL 2 excellent exon, frame 1"

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36301. 37222

/note="100% identity EST ou55c09.x1"

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36901. 37164

/standard_name="STSG-9983"

/db_xref="dbSTS:32654"

complement(37595. 33654)

/note="GRALL 2 excellent exon, frame 0"

complement(37595. 33630. 33935. 40048,40300. 40410,40503. 44507))
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1 (bases 1 to 215)
Bennett, A., Labavitch, J. M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Fatent: US 556983-A 5 29-OCT-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 HINVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKTAMTSRNRTGKTANNAVD 142
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/note="78%-100% protein identity GenPept:U18937"
comptement(18069: .38215)
comptement(18069: .38215)
comptement(180462: .38578)
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Pred. No. 3.10e-04;
56; Mismatches 59; Indels
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/note="GRAIL 2 excellent exon, frame 2" 32388. .32488
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/rpt_family="Alu"
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Sequence 5 from patent US 5569830.
128278
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32617. 32908
/rpt_family_"Alu"
32977. 33088
/rpt_family_"MLT1"
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8 c 25 g
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Best Local Similarity 12.9%;
Matches 17; Conservative
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A (Dases 1 to 74371)

Kimmarly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Davis, C.A., Kadner, K., Miguel, T., Pitluck, S., Pollard, M.,

Bojeski, H., Subramanian, S. and Martin, C.H.

Direct Submission

Submission

Institute, Lawrence Berkeley National Laboratory, MS 74-157,

Berkeley, CA 94720, U.S.A.

Sequence submitted by:

Sequence submitted by:

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_unit=Gr
join(3246.
/standard_name="Rur"
/note="65% & 69% protein identity GenPept:U22377"
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258. .8503
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11950. .12550
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9070_.9387
/rpt_family="Alu"
complement(9740..9845)
/rpt_family="MER42"
 Comparison Analysis (SCAN) System
                                                                                                                                                                                                                       /organism="Homo sapiens"
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5327. .5602
/rpt_family-"Alu"
6586. .6956
/rpt_family-"Ll"
6647. .6684
/note-"(CA)19"
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3707. .3728
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12057. .12085
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                                                                                                                                                                                                                                                                                                                      893. .1030
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2295. .2438
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2818. .2859
/note="(GT)21"
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/rpt_family="L1"
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rpt_unit=A
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                                                                                                                                                                                                                                                                       /clone="11953"
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5, BAC clone 119j3 (LBNL H175), complete
                                                                                                                                                                                                                                                                                           Unknow...
Unknown...
Unknown...
Unclassified.
1 (bases 1 to 215)
1 (bases 1 to 215)
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and their use to control fungal disease
Patent: US 5569830-A 5 29-0CT-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1616 AGTCCCGCACGTCATCCACGTCCAGCTCCAGCAGGAGCTTGGCATGCTTCCCCA 1557
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Ricke,D.O.
Large Scale Sequence Analysis and Annotation with the Sequence
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 74371)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Radner,F., Mguel,P., Miller,C., Pitluck,S., Pollard,M., Solashi,H., Subramanian,S. and Martin,C.H.
Sequencing of human chromosome 5
66 YNYGGNNVGAAKTHYYTHTNVSGADSKTVTDSYNASGTSSSNGGTDGNRSGADSYGSSKT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 AMTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGT 185
                                              143 SRNMGDASVGSDKNTKKHAKNSADGKVGSKNNGDRNNRYGTGTKSNVSNNCGGGNKRDVS 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 MSSSSVVSRTASCNDKAKKDGNTTSSWTTDCCNRTWGVCDTDTTYRVNNDSGHNKYSSAN 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 21; Length 215;
Pred. No. 8.17e-05;
76; Mismatches 95; Indels
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128278
91819054
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Homo sapiens chromosome
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Best Local Similarity 13.2%;
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                                                                                                                             251 GCACGCCGCCC 262
                                                                                                          203 SYANNKCCGSSC 214
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AC005369
g3367505
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/rpt_family="Alu"

join(29485. .29559, 29598. .29779)

// Sept. .2958 identity dbsTS:G14522 (SHGC-11312)"

// Sept. .29976
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/note="100% identity EST ov84a10.x1"
complement(30401. .30536)
/note="GRAIL 2 excellent exon, frame 2"
complement(30682. .30733)
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28712. .28930
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23202. .2336
23473. .23761
23473. .23761
23744. .23767
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14175. .14470
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complement(14906. .15259)
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15300. .15613
                                                                                                                                                              complement(16675. .16977)
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complement(16993. .17085)
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complement(17678. .18276)
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19305. .19583
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/note="(GTT7)8"

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21736. .22035

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21736. .22035

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22017. .22038

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16671. .16690
/note="(T)20"
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36901. 37222
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/dbc-"gRALL 2 excellent exon, frame 0"
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Garvin,R.T. and James,E.
Froduction of active proteins containing cystine residues
Patent: EP 0222779-A 5 20-MAY-1987;
Cangene Corporation
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Synthetic DNA for preproprotease leader & prochymosin.
A10161
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Pred. No. 3.10e-04;
46; Mismatches 25; Indels 0
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complement(34021. .34144)
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32617. 32908
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32977. 33088
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complement(31573.
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Best Local Similarity 15.5%;
Matches 13; Conservative
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Search completed: Fri Dec 25 01:59:16 1998 Job time : 23728 secs.
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1 (bases 1 to 201)

Garvin, R.T. and James, E.

Production of active proteins containing cystine residues
Patent: EP 0222279-A 2 20-MAY-1987;
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Synthetic DNA for preproprotease leader & prochymosin.
A10162
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Pred. No. 5.30e-02;
35; Mismatches 57; Indels
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Pred. No. 5.30e-02;
35; Mismatches 57; Indels
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    /organism-"Streptomyces griseus"
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1 (bases 1 to 201)

2 (arvin,R.T. and James,E.

Production of active proteins containing cystine residues
Patent: EP 022279-A 6 20-MAY-1987;

Cangene Corporation
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	Ξ	33	6.0		11	AF034173	Homo sapiens ntcon2 co	5.88e-13	
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Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Flizgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Lulu, L.-I., Marmaros, S.M., Merrick, J.M.,
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Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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EST182469 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA
                                                                                                                                                                                                                                                               Length 389;
                                                                                                                                                                                                                                                Score 385; DB 8; Lengtn Journed. No. 0.00e+00;
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1 Similarity 99.5%;
387; Conservative
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Best Local Similarity
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Fraser, C.M. and Venter, J.C. Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Cozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisser,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bioinformatics
The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699423
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hdi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6. GGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGAACTTGCGGAAGACAGTGG 120
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Pred. No. 0.00e+00;
0; Mismatches 2; Indels
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/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
<1. .>409 133 g 86 t
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Best Local Similarity 99.2%;
Matches 248; Conservative
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Sequencing Center information can be

US-08-951-733-19.rst

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AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa canda cone 97SN1787, mRNA sequence.
AA754459 92801165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified prival vector. Library went through one round of normalization, and was
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Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
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1 (bases 1 to 252)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R., Moon, E.P.,
Kim, M.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.
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                                                                    M.D., Ph.D., David Allman,
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                                                                Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allma Ph.D., Gerald Marti, M.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Mashington Diversity Genome Sequencing Clone distribution: NCI-CGAP Clone distribution: NCI-CGAP Clone distribution: NCI-CGAP Clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constructed by Bento Soares and M. Fatima Bonaldo.
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/lab_host="DH10B"
86 c 100 g 81 t
                                                                                                                                                                                                                                                                                                          Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 331.
Location/Qualifiers
                                                                                                                                                                                                                                                 www-bio.llnī.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                               Std Error: 0.00
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/clone="IMAGE:1319048"
/clone_llb="NCI_CGAP_GCB1"
Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                             Email: Robert_Strausberg@nih.gov
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Best Local Similarity 98.8%;
Matches 85; Conservative
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                                                                                                                                                                                                                        cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Cente
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortlum/Lin. at:
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Erimates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 340)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3798 ATCAGGGGATGGACTATTCCTATGTGGGGAGTGGAAGCCGGGCTCCTGGTGAGGAAAAGC 3739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA811084 340 bp mRNA EST 19-FEB-1998 oa85c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1319048, mRNA sequence.
928811084
92880695
                                                                                                                                       David Allman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 ATCTGGGGATGGACTATTCCTATGTGGGGAGTGGAAGCCGGGCTCCTGGTGAGGAAAAGC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             constructed by Bento Soares and M. Fatima Bonaldo."

/db.xref="texon:9606"

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                                                              Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allme Ph.D., Gerald Marti, M.D.
CODMA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 281.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                 ww-bio.llnl.gov/bbrp/image/image.html
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Best Local Similarity 98.8%;
Matches 83; Conservative
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Unpublished (1997)
                         Unpublished (1997)
  Tumor Gene Index
                                                                                                                                                                                                   Bonaldo, Ph.Ď.
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                                                                                                                                                                                                                     1. .252
/organism="Oryza sativa"
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/organism="Oryza sativa"
/orlitivar="Milyang3"
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vector at 5'end with EcoRI and 3' end with Xho I site."
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/lab_host="E. coll SOLR"
/lab_host="E. coll SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA754459 252 bp mRNA EST 20-JAN-1998 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cons clone 97SN1787, mRNA sequence.
AA754459 92801165
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Eukaryotae; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.

1 (bases 1 to 252)
Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P.,
Rim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
Lee, M.C. and Eun, M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
                                                                                                               Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bloserver.myongji.ac.kr
Seq primer: Ml3 Reverse Primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACATITICTGGGGGGTCATCTGTGACAGGCCTCCCTGTGCTACTCCATCCTGAAA 3211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GYWCSBBVKYHTKVSTTRATRSYTCVRKYCVMWMTKKVVKKYHVVBBGCHBTDSKCKTMW 240
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Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
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Best Local Similarity 10.0%;
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bulli, C.J., Lee, N.H., Kirkness, F.F., Weinstock, K.G., Gocayne, J.D.,
Bulli, C.J., Lee, N.H., Kirkness, F.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wei, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, M.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Noreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Fengi, D.F., Ferrie, A., Fischer, C., Hastings, G.A.,
Rozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Weil, Y.F., Whing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Franco, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of CDNA sequence
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/cultivar-"Milyang23"
/note-"Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI: Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
Tel: 82 331 290 Usur.
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bloserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Theation/Qualifiers
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a 21 c 12 g 35 t 179 others
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EST12462 Uterus tumor I Homo sapiens cDNA 5' end, mRNA sequence.
AA299878
91952209
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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Pred. No. 3.51e-49;
88; Mismatches 69;
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Best Local Similarity 12.8%;
Matches 23; Conservative
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Query Match
Best Local Similarity 14.8%;
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AA754458 92801164
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/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Vector: PBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPI:
Vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4330"
/clone="#978N184"
/clone="#978N184"
/clone=lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kynnggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Fax: 82 391 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
                                  The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
7213 9018699056
Fax: 3018699423
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seg primer: M13 Reverse.
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Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.
                                                                                                                                                                                                                                               /organism="Homo sapiens"
//organism="Homo sapiens"
//organ: uterus; Vector: pBluescript SK-; Site_1:
/db_xref="ATCC (inhost):193066"
/db_xref="Taxon:9606"
/db_tref="Taxon:9606"
/db_tref="Taxon:9606"
/db_tref="Taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                            2 others
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Pred. No. 6.91e-40;
0; Mismatches 1,
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                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                           Location/Qualifiers
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Contact: Kerlavage, AR
Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.4%;
Best Local Similarity 98.1%;
Matches 53; Conservative
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AUTHORS
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AA754458 247 bp mRNA EST 20-JAN-1998
97SNI784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
cDNA clone 97SNI784, mRNA sequence.
AA754458
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/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional CDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
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Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
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National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungqido, Korea
Tel. 82 331 290 0307
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: Mi3 Reverse Primer.
Location/Qualifiers
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Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                               243 CCTGGGACGCCCCCCCCCCCCCTCCTTCCGCCAGGTGTCCTGCTGAAGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 INTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBTAYCDYBHYBDRANHVDDTRCTNDRGYC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207
                                                                                                                                                                                                                                                   28 IBBWCCVRRVGTTINNGKHNGRTTTWNDCSDNAHCRYTVBWYYARSKYGYGTBYYSWNVD 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 NYTASDNGTSATKRVIGYDKIDSDCGGGCWRKVIYGSSBYBRCGVNVMVRITSMWIDKST
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                                                                                                                                           Length 247;
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                                                          169 others
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/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
| 16 c 21 g 34 t 169 oth
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/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
                                                                                                                                     Score 49; DB 12; 1
Pred. No. 2.37e-35;
93; Mismatches 88;
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Pred. No. 2.25e-32;
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                                                                                                                                     Query Match 1.3%;
Best Local Similarity 13.0%;
Matches 27; Conservative
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204 GTCAC 208
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DEFINITION
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TITLE
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                          AA200728 375 bp mRNA EST 19-FEB-1997 mul3h09.rl Soares 2NbMT Mus musculus cDNA clone 639329 5', mRNA
                                               3667 ITGGCTGGACACTCGCTCAGGCCTCAGCCGTCAGCCTTCAGCCGGACATGCAGGC 3608
                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                             TVBWYYARSKYGYGTBYYSWNVDTNTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBTAYCD 124
                                                                                      125 YBHYBDRANHVDDTRCINDRGYCNYTASDNGTSAIKRVIGYDKIDSDCGGGCWRKVIYGS 184
;
0
53;
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Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 361.
Location/Qualifiers
1. 375
/organism="Mus musculus"
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                              3607 CTCGGCCAAACACTCACTCAGG 3586
68;
                                                                                                                                                  SBYBRCGVNVMVRTTSMWTDKS 206
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a 95 c
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                                                                                                                                                                                                                                                                                                                                 house mouse.
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                                                                                                                                                                                                                                                                       sequence.
AA200728
g1795738
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BASE COUNT
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ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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Matches
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ų 95

b 105

80 a

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Unpublished

2 (bases 1 to 2275)

Tripodis, u. and Regoussis, J.

Direct Submission
Submitted (13-NOV-1997) Division of Medical and Molecular Genetics,
Guy's Hospital, 7th floor, Guy's Tower, London SE1 9RT, UK

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                            AF034173 2275 bp mRNA EST 22-DEC-1997
Homo sapiens ntcon2 contig mRNA, partial sequence, mRNA sequence.
AF034173
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Homo sapiens ntcon6 contig mRNA, partial sequence, mRNA sequence.
AF034177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2649 GCCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGA 2708
                                                                                                                           2448 AGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCACGCTTCATGT 2507
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 660)
Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately
                                                                                                 144 AGAGCATCTCTATGAATGAGGAGCAGCAGCAGCTGTTTGACTTCTTCCTGCACTTCCTGC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 2275)
Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
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  Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 others
Score 33; DB 23; Length 375 Pred. No. 5.88e-13; 0; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="ntcon2 contig"
/tissue_type="liver; brain"
/dev_stage="fetus"
/note="similar to Br140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1583 SSRSYWGYWGSMSGCYGMTKRYY 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2709 AAACCTTCCTCAGGACCCTGGTC 2731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.9%;
Best Local Similarity 13.3%;
Matches 11; Conservative
Query Match 0.9%;
Best Local Similarity 75.4%;
Matches 49; Conservative
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AUTHORS
TITLE
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Bult.C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Barle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fittchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kalley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Wetdman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Colleman, T.A., Collins, E.J., Dlmke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Runsch, C., Hungjun, J., Li, H., Meassner, P.S., Olsen, H., Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                AA386387 181 bp mRNA EST 22-APR-1997 EST81369 Prostate gland I Homo sapiens cDNA 5' end similar to proly1 4-hydroxylase, beta subunit/protein disulfide isomerase/thyroid hormone-binding protein, mRNA sequence. 4A386387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 181)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
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ORGANISM
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AUTHORS
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1 (bases 1 to 143)
Lee, N. H., Glodek, A., Chandra, I., Mason, T. M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus sp."
/note="Organ: muscle; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
                               bounca,
L Ompublished
S Trichases 1 to 660)
AS Tripodis,N. and Ragoussis,J.
Direct Submission
AL Submitted (13-NOV-1997) Division of Medical and Molecular General Carlon (13-NOV-1997) Division of Medical Carlon (13-NOV-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="ntcon6 contig"
/tissue_type="fetal brain; fetal liver; adult muscle"
/note="similar to CutA"
centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 143;
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Pred. No. 1.86e-10;
31; Mismatches 7; Indels
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Pred. No. 1.41e-03;
0; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 t
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/clone_lib="Normalized"
/ 49 c 58 g
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/clone="RMUBK19"
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Best Local Similarity 76.6%;
Matches 36; Conservative
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Best Local Similarity 15.6%;
Matches 7; Conservative
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Other_ESTs: TC52270
Contact: Lee, NH
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Rattus sp.
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Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.iigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse

    .181
    /organism="Homo sapiens"
    /organism="Toyan: prostate; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
    /db_xref="Arcc (inhost):174439"
    /db_xref="taxon:9606"

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                                        Bioinformatics
The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
713 13018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 6; I
Pred. No. 1.41e-03;
                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Prostate gland I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 t
                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
/dev_stage="adult, 21 yrs"
Other_ESTs: EST81368 THC170792
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n 0.7%;
Similarity 70.0%;
42; Conservative
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AA855630 187 bp mRNA ESA COMESTILL Stratagene mouse heart (#937316) Mus musculus CDNA clone 1260165 5' similar to TR:Q99960 Q99960 PLAKOPHILIN 2A. [1] ;, mRNA
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:66271
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 178.
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases I to 187)

1 stra,m., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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// Organism="Mus musculus"
// Strain="Mus musculus"
// Strain="Mus musculus"
// Strain="Mussulus"
// Str
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Pred. No. 1.41e-03;
0; Mismatches 5; Indels
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/lab_host="SOLR (kanamycin resistant)"
65 c 70 g 23 t
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The WashU-HHMI Mouse EST Project Unpublished (1996)
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Best Local Similarity 85.7%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                        house mouse.
                                                                                                                                                sequence.
AA855630
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AUTHORS
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Gaps

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Search completed: Fri Dec 25 05:48:10 1998 Job time : 13715 secs.

4 .11e-06 3..78e-0.7 1..35e-0.5 1..33e-0.5 1..33e-0.5 1..33e-0.5 1..33e-0.5 1..33e-0.6 1..33e-0.6

Signal portion of gen Streptomyces protease Substance Pantisense Human neutrophil elas HCV envelope region n

MDNCF antisense portion of gen

Generic DNA sequence
Human endothelin-1 an
Generic DNA sequence
Human RANTES antisens
Human MDNCF antisens
Human MDNCF antisens
Chymase antisens
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Human IL3 receptor an
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Human IL4 receptor an
Human IL4 receptor an
Generic DNA sequence

	c 13 3
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(IN)	1000
Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K.	
MPsrch_nna n.a n.a. database search, using Smith-Waterman algorithm with gap extension penalties as well as gap opening penalties	C 229 33 31 33
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Description: (1-3/98) from USU8951/33.seq Perfect Score: 3798 N.A. Sequence: 1 CCACGCGTCCGGCAGCGCTGGAATAGTCCATCCCTGAT 3798 Comp: GGTGCGCAGGCCCTCGCGA	
ole: TABLE d Gap ope	
Nmatch STD : Dbase 0; Query 0	
Searched: 188442 seqs, 68026449 bases x 2	
Post-processing: Minimum Match 0% Listing first 45 summaries	SUL
39:part39 40:part40 Statistics: Mean 9.981; Variance 6.350; scale 1.572	PR 26-MAY- PA (BECT) PI Shank D

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		*					
Result No.	t . Score		Query Match Length DB	DB	DI .	Description	Pred. No.
	1 45	1.2	91	6	051746	Oligonucleotide probe	2.38e-10
U	2 45	1.2	91	φ	051746	Oligonucleotide probe	2.38e-10
	3 40	1.1	114	12	970466	Generic DNA sequence	1.13e-07
υ	4 40	1.1	172	32	T76363	Human interleukin 8 a	1.13e-07
	5 43	1.1	204	-	N81164	Base substituted E.co	2.87e-09
υ	6 41	1.1	204	m	N81164	Base substituted E.co	3.34e-08
	7 39	1.0	114	12	070469	Generic DNA sequence	3.78e-07
	8 38	1.0	114	12	070468	Generic DNA sequence	1.25e-06
	9 38	1.0	114	12	070465	NA NA	1.25e-06
0	0 38	1.0	114	12	070465	DNA &	1.25e-06
C	1 38	1.0		12	970468	Generic DNA sequence	1.25e-06
0	2 38	1.0		12	970467	DNA	1.25e-06

RESULT

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		for MK14 but	Gaps 60 445
	is;	ised in of ced, may	0; vsv (
	T 1 051746 standard; cDNA; 91 BP. 051746; 31-MAY-1994 (first entry) 011gonucleotide probe MK14-A 011gonucleotide; DNA probe; mycobacteria; disease diagnosis; synthetic. EP-571911-A. 01-DEC-1993. 24-MAY-1993; 108325. 25-MAY-1992; US-889651. (BECT) BECTON DICKINSON CO. Shank DD. Spears PA;	New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in samples  Claim 3: Page 14; 23pp; English.  Claim 3: Page 14; 23pp; English.  Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14 (Oli735). It hybridized to all spp. of mycobacteria tested, but cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection.  See also Q51735-45 and Q51747-59.  Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;	y Match Local Similarity 7.3%; Pred. No. 2.38e-10; hes 4; Conservative 46; Mismatches 5; Indels 0; G cggcgssvhsyyvhvvshhhsvhhvvhhvhsvvvvhhvvhhvhyhyvsv 60
	e e e e	obacter nucleic leotide bacteri The rial in	Leng 10; 5; vvhvvh : :::
	ia; d1:	or Mycoteria of nucof mycol appropriate of nucolar spp	DB 9; 2.38e- tches vvvvhh:::::
ALIGNMENTS	obacter	Specific for Mycobac lish.  Ish.  consists  all spp. c  robacteri en for myc  7-59.	Score 45; DB 9; L Pred. No. 2.38e-10; h4v6; Miswatches 5 hnvvhnvhvsvvvvhhvvh ::::::::::::::::::::::::::
ALIG	A A myco	speriof 1	Sco. Pre 46; 46; whhy
	051746 standard; CDNA; 91 BP. 051746; 31-MAY-1994 (first entry) 014gonucleotide; DNA probe; mss. 014gonucleotide; DNA probe; mss. Synthetic. EP-571911-A. 01-DEC-1993. 24-MAY-1992; US-889651. (BECT ) BECTON DICKINSON CO. Shank DD, Spears PA;	New oligo: nucleotide probes speci detection and amplification of My samples Samples Claim 3: Page 14: 23pp; English. Oligonucleotide probe MK14-A cons (OS1735). It hybridized to all s cross reacted to a few non-mycoba be useful as an initial screen fo See also OS1735-45 and OS1747-59. Sequence 91 BP: 5 A: 17 C	1.2%; 7.3%; ative rvshhhs ::::::
	rd; cDNi (first e de probede; DNA 108325. US-88965 NN DICKII	amplifi eotide 14; 23 probe to a fe 5-45 ar	1.2% imilarity 7.3% 4; Conservative gssvhsyyvvhvvshh  :::::::::::::::::::::::::::::::::::
	D51746 standard; cDNA; 91 051746; 31-MAY-1994 (first entry) 011gonuclectide probe MKI4 olligonuclectide; DNA probe Ss. Sy. C.	Page 14; Page 14; leotide pi acted to bacted t	Ouery Match Best Local Similarity Matches 4: Consea  6 cggcgssynsyyv 6 cggcgssynsyyv 1
	051746 standa 051746; 31-Max-1994 011gonuclecti 011gonuclecti 011gonuclecti Syrthetic. EP-571911-A. 01-DEC-1993. 26-Max-1992; CBECT ) BECTC Shank DD.	Mer, 95 detection detection samples Claim 3; 01igonuci cross res cross res cross res cross res cross res cross res cross res cross res	Query Match Best Local : Matches 6 cgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identifying proteins or peptide(s) which bind a ligand - by
recenting a recombinant vector library expressing fusion proteins
recombinant vector library expressing fusion proteins
recomprising a binding domain and an effector domain
bisclosure; Page 35; 255pp; English.
C 70466 is a generic DNA sequence used to generate random TSAR (Totally
Synthetic Affinity Reagents) peptides. This generic formula can also be
represented as follows:X(NNB)1(TGC) (NNB)10(TGC)2(NNB)4Z(NNB)8(TGC)(NNB)
C 9Y. X and Y are flanking restriction sites (X is not the same as Y)
that are not specified further. Other generic sequences are shown in
Q70466-68. Other specific peptides generated by these generic sequences
are shown in R65151-54. TSARs are concatenated heterofunctional proteins
or peptides, comprising at least two functional regions - a binding
domain with affinity for a ligand and a second effector peptide portion
that is chemically or biologically active. They may further comprise a
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                          Generic DNA sequence to generate a random TSAR-9 petide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                         4 tccggcgssvhsyyvvhvvshhhsvhhvvhvhhvhvvhvvhhvhhvhyhvyvsvct 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ľΩ
                                                                                                                                                                                     New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          þ
                                                                                                                                                                                                                           claim 3; Page 14; 23pp; English.
Oligonuclectide probe MK14+A consists of nuclectides 5-95 of 1016ponuclectide probe MK14+A consists of mycobacteria tested, 167035). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. Sequence 91 8P; 5 A; 17 C; 15 G; 4 T;
                      31-MaY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          can
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                                                                                                                                                                                                                                                                                                                                     Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "this sequence represents 'Z'; Z sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                                                                                                                                       Score 45; DB 9; LA Pred. No. 2.38e-10;
                                                                                                                                                                                                                                                                                                                                                                 45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 3
Q70466 standard; DNA; 114 BP.
Q70466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "this
                                                                                                                    24-MAY-1993; 108325.
26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
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                                                                                                                                                                                                                                                                                                                                     Query Match 1.2%;
Best Local Similarity 11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comments)"
standard; cDNA; 91
                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
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                                                                                                                                                           Shank DD, Spears PA;
WPI; 93-378844/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kay BK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994;
                                                                                          EP-571911-A.
01-DEC-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                         Shank DD,
                                                                            Synthetic
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linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARS or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eq. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyronal antibodes and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARS are easily characterised and have designed activity allowing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:| | :|:::|: || :| || :| || 3487 CIGGCIGIGGCCGGGTCCAGGATGCICITGAAGTCTGAGGGCAGTGCCGG 3428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 gtbggtcbgbbbgbtgtgcttbccttcbcbcbgbgctgcbgbbbtcbggbbggctgccbb 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 bccbbbgcbtcbbgbbtbgctttgctbtctbbggbtcbcbtttbgbcbtbggbbbbcgct 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 btgcnnbnnbnnbnnbnnbnnbnnbnnbnnbtgctgcnnbnnbnnbnnbnnnnnn 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bronchoconstriction in patients with hyper-reactive airways 172 BP; 0 A; 35 C; 42 G; 39 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 banbanbanbanbanbanbanbtgcanbanbanbanbanbanbanbanbanb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-5EP-1997 (first entry)
Human interleukin 8 antisense oligonucleotide.
Asthma; airway epithelium; adenosine free; cystic fibrosis; chronic obstructive pulmonary disease; bronchitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 32; Length 172;
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Pred. No. 1.13e-07;
52; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 12; Length 114
Pred. No. 1.13e-07;
32; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 4 C; 4 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gbgbgccbcggccbgcttggbgtcbtgtttbcbcbcbg 168
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06-JUN-1996, U09306.
07-JUN-1995, US-474497.
(UYEC-) UNIV EAST CAROLINA.
METZGET WJ, NYCE JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.1%;
Best Local Similarity 8.9%;
Matches 10; Conservative
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Best Local Similarity 29.7%;
Matches 47; Conservative
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RESULT

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Introducing random point mutations into nucleic acods -
Introducing random point mutations into nucleic acods -
Introducing random stranded template, annealing a primer, elongation,
maisincorporation, completion of molecules and screening.
Bisclosure: p; English.
Random point mutations were introduced into the alpha fragment of
E.Coli beta-galactosidase. The wild type sequence was obtained as a
single stranded template and an oligonuclectide was hybridised to
it to generate a popn of DNA molecules which terminate at all
possible nuclectide positions within a specified region. The
voriable 3' ends generated in this way are used as primers for
reverse transcriptase. Nuclectides are misincorporated by the
transcriptase and the molecules are completed to forms that can be
amplified and then expressed in a suitable host-vector system.
The sequence covers all 176 diffit base substitutions, most of which
see also P80575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOURTON DAY, MAY DAY, WPI; 94-27939/34.

Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure; Page 35: 255pp; English.

070469 is a generic DNA sequence used to generate random TSAR peptide This generic Commula can be represented as follows: X(TGC)(NNB)10-(TGC)(NNB)5Z(NNB)2(TGC)(NNB)14(TGC)x x and Y are flanking restriction sites (X is not the same as Y) that are not specified further. This sequence generates peptides that are cloverleaf in structure. Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2034 GAGGIGAGACGCICCGCCCCTCTTTCTCTGCGGAACGTTCTGGCTCCCACGACGTAGTCC 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 aaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncncccbnnhvchnvhbnnh 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 aggnyccccggggywccgagcycgaayycdchvgccgymrttthhyrrmrbnvyrdynrsd 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
Synthetic.
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/note= "this sequence represents '2'; 2 can
sequence of 6,9 or 12 nucleotides (see
comments)"
                                                                                                     Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.1%; Score 41; DB 1; Length 204; Best Local Similarity 18.8%; Pred. No. 3.34e-08; Matches 27; Conservative 58; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1974 AIGITCACAATCGGCCGCAGCCCG 1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 rnwayvrhdarrddvhccvchccg 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994; U00977.
01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           070469 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 A;
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07-APR-1995 (first entry)
                                                                  (SUSO) SUOMEN SOKERI OY.
                                      ; US-034819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; promitted in the course and screening.

Bandom point mutations were introduced into the alpha fragment of Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligomoucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which cocurred singularly in any given mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        890 CCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCCTTGGCACGCGCAC 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 ynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncncccbnnhvchnv 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bcyrraggnyccccgggywccgagcycgaayycdchygccgymrttthhyrrmrbnvyrd 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation, misincorporation, completion of molecules and screening.
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08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                             N81164;
08-NOV-1990 (first entry)
asse substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 T;
3427 GITGGCTGCGGCCTCCAGGGCAGTCAGCGTCGTCCCCG 3390
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/function=multiple cloning site
187.204
/*tag= b
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//function=multiple cloning site
187.204
/*tag= b
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Pred. No. 2.87e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 C;
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                                                                                          T 5
N81164 standard; DNA; 204 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 1.1%;
Local Similarity 20.9%;
nes 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19..69
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30-MAR-1988; 105163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 BP;
                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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05-MAY-1988.
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Sequence Query Match Matches 45

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Gaps

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108 Others;

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generic sequences are shown in 070465-68. Other specific peptides

generated by these generic sequences are shown in R65150-54. TSARS are
concatenated heterofunctional proteins or peptides, comprising at least
two functional regions - a binding domain with affinity for a ligand and
a second effector peptide portion that is chemically or biologically
active. They may further comprise a linker peptide between the 2 domains.

The oligonucleotides are also designed so that the expressed peptide
contains 2 or 4 cysteine residues positioned in, or flanking, the
unpredicted or variant residues. These residues confer some degree of
conformational rigidity to the peptides. The TSARS or comparising
a TSAR binding domain can be used in vivo to deliver a chemically or
biologically active moiety, eg. metal ion, radioisotope, peptide, toxin
c renzyme, to the specific target or on the cell. They can also replace
the function of macromolecules, eg. monoclonal or polyclonal antibodies
and therefore circumvent the need for complex methods of hybridoma
formation or in vivo antibody production. The TSARs are easily
detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Terebash rost-tier.

Tentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain.

Screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain.

Solution and the sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)1(TGC)(NNB)5(Z(NNB)7(TGC)(NNB)10Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.

Other specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with a filinity for a ligand and a second effector peptide portion that is chemically or biologically active they may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so
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TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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//tag= a
//note="this sequence represents '2'; 2 can be sequence of 6, 9 or 12 nucleotides (see comments)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 12;
Pred. No. 3.78e-07;
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Q70468 standard; DNA; 114 BP.
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ilarity 7.2%;
Conservative
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31-JAN-1994; US-189331.
(UTNC-) UNIV NORTH CAROLINA.
FOWIKES DM, RAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q70468;
05-APR-1995 (first entry)
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US-176500.
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Best Local Similarity
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Terbuis rolling and Rolling which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PT Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins

PT comprising a binding domain and an effector domain

Disclosure; Page 35; 25pp; English.

CQ 0465 is a generic DNA Sequence used to generate random TSAR (Totally

CG 070465 is a generic DNA Sequence used to generate can also be

represented as follows: x(NNB) [GGC) (NNB) 112 (NNB) 14 (TGC) (NNB) 3Y. x

and Y are flanking restriction sites (X is not the same as Y) that are

CC and Y are flanking restriction sites (X is not the same as Y) that are

CC other specified further. Other generic sequences are shown in Q70466-68.

CO ther specified further or generic sequences are shown in CR65151-54. TSARs are concatenated by these generic sequences are shown in

CR65151-54. TSARs are concatenated beterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with

CC affinity for a ligand and a second effector peptide portion that is

CC chartly for a ligand and a second effector peptide portion that is

CC that the expressed peptide contains 2 or 4 cysteine residues positioned

CI no or flanking, the unpredicted or variant residues. The TSARS

CC confer some degree of conformational rigidity to the peptides. The TSARS

CC confers comprising a TSAR binding domain can be used in vivo to

Cdelliver a chemically or biologically active moiety, eg. metal ion,

C addioisotope, peptide, toxin or enzyme, to the specific target or on the

CC cell. They can also replace the function of macromolecules, eg.
that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 GGGGGCCTGGGGCCCCAAGGGCTGGCGGCTGGTGCAGCGCGGGGGACCCGGCGGCTTTCCGC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             070465;
05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                    3 banbanbanbanbanbanbanbanbanbtgcanbanbanbanbanbanbannann 62
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//note= "this sequence represents '2'; Z can be
sequence of 6, 9 or 12 nucleotides (see
comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 bnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 GCGCTGGTGGCCCAGTGCCTGGTGCCTGCCTGGGACGCACGGCCGCCCC 263
                                                                                                                                                                                                                                                                                                                                  Length 114;
                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.25e-06;
34; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                    DB 12;
                                                                                                                                                                                                                                                                                                                                       Score 38;
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Q70465 standard; DNA; 114 BP
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                                                                                                                                                                                                                                                                                                                                  1.0%;
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P-PSDB; R65150 and R65151.
                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994; U
01-FEB-1993; U
30-DEC-1993; U
31-JAN-1994; U
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Pred.

Best Local Similarity

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Tentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; Page 35: 255pp English and in a frector domain bisclosure; Page 35: 255pp English and in a frector domain bisclosure; Page 35: 25pp English and in a factor formula can also be represented as follows: X(NNB) 6(TGC)(NNB)112(NNB)14(TGC)(NNB)3Y. X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68. Other specified further of the specified for a ligand as a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in or flanking the unpredicted or variant residues positioned in or flanking a flower some degree of conformational rigidity to the peptides. The TSARS conformation of the specified or the specified and the standard and a second effector peptides. The TSARS conformation of the specified or variant residues. The TSARS conformation or the specified or the specified compans.
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                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                          2491 CTTCCTACGCTTCATGTGCCACCACGCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG 2550
monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing for and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                        2551 CCAGGGGATCCCGCAGGCTCCATCCTCCACCGCTGCTCTGCAGCCTGTGC 2602
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/note= 'this sequence represents '2'; 2 can
sequence of 6, 9 or 12 nucleotides (see
comments) "
                                                                                                                                                         Length 114;
                                                                                                                                                                                                      73; Indels
                                                                                                                                                      Score 38; DB 12; I
Pred. No. 1.25e-06;
33; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JT 10
Q70465 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Ray BK;
                                                                                                                                                      1.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      070465;
05-APR-1995 (first entry)
                                                                                                                                                                                                         6; Conservative
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/*tag=
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30-DEC-1993; US-176500.
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                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                      Matches
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Length 114;

DB 12;

Score 38;

1.0%;

Query Match

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Terbil Robles

PT Februs

PT Identifying proteins or peptide(s) which bind a ligand - by

Screening a recombinant vector library expressing fusion proteins

PT Comprising a binding domain and an effector domain

Disclosure; Page 35; 255pp; English .

COMPAGE is a generic DNA sequence used to generate random TSAR (Totally Spinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)1/(TCC)(NNB)2/(TCC)(NNB)100; X and Y are flanking restriction sites (X is not the same as Y) that are cont specified further. Other generic sequences are shown in 707046-68.

CC offers specific peptides generated by these generic sequences are shown in 85151-54. TSARs are concatenated heterofunctional proteins or peptides, CO ther specific peptides generated by these generic sequences are shown in 85151-54. TSARs are concatenated heterofunctional proteins or peptides, CO comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker of faming, the unpredicted or variant residues. These residues to that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confers some degree of conformational rapidity to the peptides. The TSARs or comprising a TSAR binding domain can be used in vivo to confers some degree of conformation or enzyme, to the specific target or on the conformation or polyclonal antibodies and therefore circumvent the need conformation and rapid detection in a screening process.

Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
                                                                                                         1528 GAAGCGGCGTTCGTTGTGCCTGGAGCCCTGGGGGCCTGGGGGCACCAGCCGGCGCAGGCA 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1543 CTTGGTGTTTCCTGAGGAAGCGGCGTTCGTTGTGCCTGGAGCCCCAGAGGCCTGGGGGGCAC 1484
                                                                                                                                                                                                                                                                                                                              Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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34; Mismatches 73; Indels
No. 1.25e-06;
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/note= "this sequence represents '2'; Z
sequence of 6, 9 or 12 nucleotides (see
comments)"
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                              Mismatches
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                                                                                                                                                                                                                                                                      BP.
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Fowlkes DM, Kay BK;
WPI; 94-279739/34.
P-PSDB; R65154.
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Best Local Similarity 4.5%;
Matches 5; Conservative
            larity 4.5%;
Conservative
                                                                                                                                                                                                                                                                                                           05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                      standard; DNA; 114
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US-189331.
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31-JAN-1994;
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Q70468;
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070469;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              rdentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English.

C70467 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)[GTGC](NNB)12(NNB)16(TGC)(NNB)12, X and Y are flanking restriction sites (X is not the same as Y) that are not specified further. Other generic sequences are shown in Q70466-68.

Cher specific peptides generated by these generic sequences are shown in R5151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with comprising at least two functional regions - a binding domain with the chancally or biologically active. They may further comprise a linker the light between the 2 domains. The oligonucleotides are also designed so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromalecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; reffector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
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/note= "this sequence represents 'Z'; Z can be
sequence of 6, 9 or 12 nucleotides (see
comments)"
                            1483 CAGCCGCCGCCAGGCCCGCACGAAGCCGTACACCTGCCAGGGGCTGCTG 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 bnabnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnb 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.0%; Score 38; DB 12; Length 114; 4.5%; Pred. No. 1.25e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73; Indels
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                                                                                                                                                                                                                     Location/Qualifiers
                                                             LT 12
Q70467 standard; DNA; 114 BP.
Q70467;
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Fowlkes DM, Kay BK;
WPI; 94-279739/34.
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Matches 5; Conservative
                                                                                                                        05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                         01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
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                                                                                                                                                                                                                                    misc_feature
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Well 94-1/9/30/44.

Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins PT Genering a recombinant vector library expressing fusion proteins PT comprising a bluding domain and an effector domain bisclosure; Page 35; 255pp; English.

Disclosure; Page 35; 255pp; English.

CT G704(69 is a generic DNA Sequence used to generate random TSAR peptide CT This generic Cormula can be represented as follows; KTGC)(NNB)10-CT GTGC)(NNB)2(TGC)(NNB)14(TGC)Y. A and Y are flanking restriction sites (X is not the same as Y) that are not specified further. This scapuence generates peptides that are cloverleaf in structure. Other corrected by these generic sequences are shown in Q70455-68. Other specific peptides

CC Generated by these generic sequences are shown in M70455-68. Other specific peptides

CC Generated by these generic sequences are shown in A70455-69. Other specific peptides

CC Generated by these generic sequences are shown in A70455-69. Other specific peptides

CC Generated by these generic sequences are shown in A70455-69. Other a ligand and a second effector peptide portion that is chemically or biologically or biologically are also designed so that the expressed peptide

CC concatains 2 or 4 cysteine residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsens. Comprising a TSAR binding domain can be used in vivo of celliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or engage in vivo antibody production. The TSARs are easily conformated in a screening process.

CC Characterised and have designed activity allowing direct and rapid detection in a screening process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3572 GCGGTGCGGGCCTGGGTGTGGGCCGCCCCTCCCTCGGGACGTAGAGCCCGGCGTGAC 3513
                            Generic DNA sequence to generate a random TSAR peptide library.
TSAR: totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concateneated heterofunctional protein; linker;
direct: rapid; detection; screening; treatment; generic; ss.
Synthetic.
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/*tag a
/note= "this sequence represents 'Z'; Z can |
sequence of 6,9 or 12 nucleotides (see
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Human endothelin-1 antisense oligonucleotide.

Asthma; airway epithelium; adenosine free; cystic fibrosis;

Chronic obstructive pulmonary disease; bronchitis; ss.

W09640162-A1.
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Pred. No. 4.11e-06;
32; Mismatches 72; Indels
                                                                                                                                                                                                        Location/Qualifiers
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T76405 standard; DNA; 178 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN 1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, KAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.3%;
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07-APR-1995 (first entry)
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US-189331.
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Best Local Similarity
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or 13 070469 standard; DNA; 114 BP.

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Subject Claim 5; Page 38; 71pp; English.

Claim 5: Page 38; 71pp; English.

C A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithalium of the free antisense oligonucleotide specific of the human endothelio-1, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary diseases, bronchits and other caliway diseases characterised by an inflammatory response. By climinating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-continuous antisense degradation in patients with hyper-reactive airways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                            A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonuclectide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonuclectide specific for the human endothelin-1, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary diseases, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-reactive airways. Sequence 178 BP; O A; 52 C; 46 G; 32 T;
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                                 07-JUN-1995; US-474497.
(UYEC-) UNIV EAST CAROLINA.
Metzger WJ. Nyce JW:
WPI: 97-051871/05.
Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asthma; airway epithelium; adenosine free; cystic fibrosis; chronic obstructive pulmonary disease; bronchitis; ss.
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Pred. No. 1.25e-06;
41; Mismatches 40; Indels
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T76405 standard; DNA; 178 BP.
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07-JUN-1995; US-474497.
(UYEC-) UNIV EAST CAROLINA.
Metzger WJ, Nyce JW;
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Matches 22; Conservative
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A method for treating a
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Search completed: Fri Dec 25 06:17:23 1998 Job time: 1733 secs.

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16 1520 40.0 2171 21 US-08-846- Sequence 100, Applicatio 0.00 17 1497 39.4 4200 22 US-08-912. Sequence 16, Applicatio 0.00 18 1079 28.4 3496 23 US-08-915. Sequence 18, Applicatio 0.00 535 14.1 550 22 US-08-911. Sequence 52, Applicatio 0.00 22 US-08-911. Sequence 52, Applicatio 0.00 22 US-08-911. Sequence 52, Applicatio 0.00 22 US-08-911. Sequence 62, Applicatio 0.00 23 385 10.1 389 21 US-08-846. Sequence 62, Applicatio 0.00 25 385 10.1 389 21 US-08-844. Sequence 62, Applicatio 0.00 27 385 10.1 389 22 US-08-811. Sequence 62, Applicatio 0.00 27 385 10.1 389 22 US-08-912. Sequence 62, Applicatio 0.00 27 385 10.1 389 22 US-08-912. Sequence 62, Applicatio 0.00 27 389 22 US-08-912. Sequence 63, Applicatio 0.00 27 389 22 US-08-912. Sequence 17, Applicatio 0.00 28 32 32 32 32 32 32 32 32 32 32 32 32 32	ALIGNMENTS  SULT  US-08-951-733-19 STANDARD; DNA; UNC; 3798 BP.  XXXXXX  SEQUENCE 19, Application US/08951733  SEQUENCE 19, Application US/08951733  APPLICANT: Robinson, Murray O.  TITLE OF INVENTION: NOVEL GENES ENCODING TELOMI NUMBER OF SEQUENCES: 44  CORRESPONDENCE ADDRESS:	CC STREET: Amagen Inc. CC STREET: One Amagen Center Drive CC CITY: Thousand Oaks CC CITY: Thousand Oaks CC COUNTRY: USA CC COMPUTER: CA CC COMPUTER READABLE FORM: CC COMPUTER READABLE FORM: CC COMPUTER: IBM PC COMPATIBLE CC COMPUTER: TBM PC COMPATIBLE CC COMPUTER: TBM PC COMPATIBLE CC COMPUTER: TAPE: TBM PC COMPATIBLE CC COMPUTER: TAPE: TBM PC COMPATIBLE CC COMPUTER: TAPE: TA
######################################	Scoring table: TABLE default  Gap open 30; Gap extend 1  Nmatch STD: Dbase 0; Query 0  Searched: 1665728 seqs, 535777161 bases x 2  Post-processing: Minimum Match 0%  Listing first 45 summaries  Database: n-pending	## Score of the cotal score of the result being printed, and is derived by analysis of the total score distribution.  **Score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  **Score Match Length DB ID

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Pred. No. 0.00e+00;
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TELEFAX: (805) 499-8011
INFORMATION FOR SEQ ID NO: 19:
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3798 BP; 613 A; 1310
           SEQUENCE CHARACTERISTICS:
LENGTH: 3798 base pairs
TYPE: nucleic acid
                               single
                                                            Query Match
Best Local Similarity 100.0%;
Matches 3798; Conservative
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APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Raren B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcripta
NUMBER OF SEQUENCES: 170
CORRESONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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Sequence 1, Application US/08911312
GENERAL INFORMATION:
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ON STANDARD; DN

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C SEQUENCE 1, APPLICATION US/C

C SEQUENCE 1, APPLICATION US/C

C GENERAL INFORMATION:

CC APPLICANT: Cech, Thomas

CC APPLICANT: Chapman, Kare

CC APPLICANT: Chapman, Kare

CC APPLICANT: Chapman, Kare

CC APPLICANT: Maraura, TO

CC APPLICANT: Andrews, Will

CC APPLICANT: ANDRESS: 17C

CC CORRESPONDENCE ADDRESS:

CC CTIT: SAN Francisco

CC STATE: California
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184 GCAGCGGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGTGGGTGCC 243
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OTHER INFORMATION: /product= "human telomerase reverse OTHER INFORMATION: transcriptase (hTRT)"
OTHER INFORMATION: /note= "cDNA contained in plasmid OTHER INFORMATION: pGRN121"
SEQUENCE 7029 BP; 1416 A; 2122 C; 2051 G; 1440 T; 0 OTHER.
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Pred. No. 0.00e+00;
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                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 013389-002500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION APAR:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                    APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-02T-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Einhorn, Gregory P. REGISTRATION NUMBER: 38,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 7029 base pairs TYPE: nucleic acid
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Best Local Similarity 99.9%;
Matches 3791; Conservative
         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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CAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACGCCGTGCG **AACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAA** CTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCT TCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACAC CGCCGGCCCTCTGCCCTCCGAGGCCGTGCGAGTGGCTGTGCCACCAAGCATTCCT GGCACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAG GGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCCAC CTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCG GCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCA GAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTT GATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGAC GGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCAC CTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCT GCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGC GCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGC

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3724 TCCACCCAGGCCAGCTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAAT 3783
                                                                                                                              CGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAG 4377
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APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas T.
APPLICANT: Nakamura, Toru
APPLICANT: Marin, Gregg B.
APPLICANT: Marin, Gregg B.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, William H.
APPLICANT: Andrews, Milliam H.
APPLICANT: Andrews, Milli
                                                     CGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAG
                                                                                                                                                                                                       CCAAGGGCTGAGTGTCCAGCACATGTCCTTCACTTCCCCACAGGCTGGCGCTCGGC
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APPLICATION NUMBER: US/09/052,919
FILING DATE: 31-MAR-1998
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
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FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
FILING DATE: 06-MAY-1997
FILING DATE: US 08/851,843
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US-09-052-919-1 STANDARD; DNA; UNC; 4015
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FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
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FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 1, Application US/09052919
GENERAL INFORMATION:
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OTHER INFORMATION: /Product= "human telomerase reverse OTHER INFORMATION: transcriptase (html)"
SEQUENCE 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 OTHER.
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Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Parent, Annette S. REGISTRATION UNIMERS. 42,058
REFERENCE/DOCKET UNIMER: 015389-003600US
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: WO PCT/US97/17885 FILING DATE: 01-OCT-1997 ATTORNEY/AGENT INFORMATION:
                                                           APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
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STRANDEDNESS: single
                                         PRIOR APPLICATION DATA:
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433	CIGCECAACACGGIGACCGACGCACIGCGGGGGGGGGCGTGGGGGGCTGCTGCTGCG	ପ୍ର	1561
481	CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGACGCTGCGCGCCCTTTTGTGCTGGT 540	. Oy	1573
١ <	CY 0x C C THE C C C C C C THE C C C C C C C C C C C C C C C C C C C	q _Q	1621
553		Qy	1633
601	CCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGC 66	g Q	1681
613	CAGGCCCGGCCCCCCCACACCCTAGTGGACCCCGAAGGCGTCTGGGATGCGAAGGGC 57.	Qy	1693
199	77 Deput	අු	1741
673	1 m	Qy	1753
721	ののののであるのであるのである。 マー・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・	đ	1801
733	ა თ	Qy	1813
781	AGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCGGGCAGGAC 84	qa	1861
793		δλ	1873
· 4	00	QQ —	1921
853	STEGACCCAGTGACCGTGGTTTCTGTGTGGTCACCTGCCAGACCGCCGAAGAAGC 91	Qy	1933
901	TGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCATCCGTGGGCCGCCA 96	qq	1981
913	7	QY	1993
961	GGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCTTGTCC 10	qq	2041
973	03	δō	2053
1021	10	අධ	2101
1033	CCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAGCTGCG 1092	δλ	2113
1081	GCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA 1140	අ 	2161
1093		O _y	2173
1141	CTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCT 120	qq	2221
1153	21	QY	2233
1201	TACTEGECANATICEGECTOCTETTTCTGCAGCTTGCAACCACGCGCA 126	qa	2281
1213	TITLE TO THE TOTAL THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TOTAL TO THE TO	Qy	2293
1261	SCCCTACGGGGGCCTCTCAAGACGCACTGCCGGCTGCGAGCTGCGGGTCACCCCAGC 132	q _Q	2341
1273	7	δλ	2353
1321	TGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAAGA	qq	2401
(2)	139	QY	2413
1381	CGTCGCCTGGTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTA 144	qa	2461
1393	145	δλ	2473
1441	SCGCCGGCTGCTCCCAGGCCTCTGGGGCTCCAGGCA 15	qa	2521
1453		Qy	2533
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CAAGTIGCAAAGCATIGGAAICAGACAGCACITGAAGAGGGIGCAGCIGCGGGAGCIGIC CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC CAGCGTGCTCAACTACGAGCGGGGGGGGCGCCCCGGGCTTCCTGGGCGCCTCTGTGCTGGG CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA GACCAGCCCCCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCCAG CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG CAAGTCCTACGTCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG

CAGCCTGTGCTACGGCGACATGGAGAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT

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3733 GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3792
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION WUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
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FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                     US-08-912-951-1 STANDARD; DNA; UNC; 4015
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STATE: California
COUNTRY: United States of America
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08912951
Sequence 1, Application US/08912951
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                               3781 CCAGAT 3786
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                                                                                                                                                          GCCGCCCACGACTATTCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGT
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                                               GCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCCACGCGAAAAC
                                                                                                                                                                                                                             GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT
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                                                                                                  Length
                                                                                                Score 3784; DB 22;
Pred. No. 0.00e+00;
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56.3454
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OTHER INFORMATION: /product= "htrr"
OTHER INFORMATION: /note= "human telomerase revers
OTHER INFORMATION: transcriptuse (htrr) catalytic
OTHER INFORMATION: component"
SEQUENCE 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 OTHER.
                                                                                             #1.30
                                                                                                                                                                                                                                                                                                                ATCORNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 3784; DB 21;
Pred. No. 0.00e+00;
0; Mismatches 1;
                                                             MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILLING DATE: 09-MAY-1997
 8th
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIPICATION: 536
                                                                                                                                                         APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
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APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
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  Center,
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  Two Embarcadero
                    California
: United States
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Best Local Similarity 100.0%;
Matches 3785; Conservative
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           San Francisco
                                                COMPUTER READABLE FORM MEDIUM TYPE: Floppy
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LOCATION: 56.
                                COUNTRY:
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MEDIUM TYPE: Floppy disk
COMPUTER: BW PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,981
FILING DATE: 20-FEB-1998
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 60/064,322
FILING DATE: 30-CT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/064,322
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,762
FILING DATE: 10-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/047,151
FILING DATE: 20-MAY-1997
PRIOR APPLICATION NUMBER: US 60/047,151
FILING DATE: 20-MAY-1997
PRIOR APPLICATION NUMBER: US 60/038,750
FILING DATE: 20-FEB-1997
APPLICATION NUMBER: US 60/038,750
FILING DATE: 20-FEB-1997
ATONNEY/AGENT INPORMATION:
NAME: CAPANAN
                                                                                                                                                                                                                                                                Sequence 35, Application US/09026981
Sequence 35, Application US/09026981
GENERAL INFORMATION:
APPLICANT: Counter, Christopher M.
APPLICANT: Meyerson, Matthew
APPLICANT: Meyerson, Matthew
APPLICANT: Meinberg, Robert A.
TITLE OF INVENTION: Telomerase Catalytic Subunit (NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                 Brook, Smith & Reynolds,
                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Granahan, Parricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH197-11p4AM
TELECOMMUNICATION INFORMATION:
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US-09-026-981-35 STANDARD; DNA; UNC; 4023
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STREET: Two Militia Drive
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TELEFAX: 781-861-9540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 TGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCTGGCGGCTGGTGCAGCGCG
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                                                                                                 Length 4023
                                                                                                                           Indels
                                                                    C; 1277 G; 715 T; 0 OTHER
                                                                                              Score 3781; DB 23;
Pred. No. 0.00e+00;
0; Mismatches 3;
SEQUENCE CHARACTERISTICS:
LENGTH: 4023 base pairs
                                                                     SEQUENCE 4023 BP; 668 A; 1363
                                                                                              Query Match
Best Local Similarity 99.9%;
Matches 3784; Conservative
                           TYPE: nucleic acid
STRANDEDNESS: single
                                                         linear
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δ	912 (	CCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCATCCGTGGGCCGCC 971	i	
QQ	963 7	;CGGGCCCCCCATCCACATCGCGGCCACGTCCCTGGGACACGC	a	2043 TC
ò	972 1	7	Qy	22
qq	1023 (	TGTACGCCGAGACCAAGCACTTCCTCATCTCCTCAGGCGACAAGGAGCAGCTG	අ	2103 GC
ò	~		Qγ	2112 GC
1 6	~	- ジョンション・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・	QQ	2163 CG
3 8	. ~	or ∟C	Qy	2172 CG
7 2		**************************************	QQ	2223 AG
3 8			Qy	2232 AG
7 2		りで、	QQ	2283 G1
3 8	1212		δy	2292 GT
; a		137	qa	2343 AC
δ	72	133	Qy	352
qq	1323 (	TCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAG	qa	2403 AG
ò	332	3 6	QY	2412 AG
- d	<u>۳</u>	**************************************	q	2463 GC
ò	392	145	Qy	2472 GC
. a	443	CGTGCGGGCCTGCGCGGCTGCTGCCCCAGGCTTGCGGCTTTGGGGGCTCCAGGC 15	qq	2523 GC
ò	~	5 2	Qy	2532 GC
;		リュー・ペンション・ション・ション・ション・ション・ション・ション・マイ・マー・マー・マー・マー・マー・マー・マー・マー・マー・マー・マー・マー・マー・	qa	2583 GC
8 8	512	57	Qy	2592 GC
q	m	TGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTTGCGCTTGCGCA 162	qa	2643 TG
ò	572	163	Qy	
· ф	m	GGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGG 168	qa	2703 CC
ò	632 (	GAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGAATCCTGG 169	Qy	2712 CC
1 2	683	1 2 1	q	2763 AG
ò	692	75	Qy	2772 AG
qq	1743 1	18	qq	2823 TG
Qy	22	83	QY	2832 TG
g	1803 (	GCAAGTIGCAAAGCATIGGAAICAGACAGCACTIGAAGAGGGIGCAGCIGCGGGAGGIGT 1862	qa	2883 TG
. ò	12		QŸ	2892 TC
g Q	863 (	GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCC	qa	2943 GC
δ	72 (	93	QY	2952 GC
qq	1923 (	CCAAGCCTGACGGGTGCGGCCGATTGTGAACATGGACTACGTGGGA	qa	3003 G1
δ	1932 (		ογ	012
qq	1983	CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTG	Q C	90
δ·	1992 (		ò	3072 AC
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GCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGG GACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCA GCTCCTGCGTTTGGTGGATGATTCTTGTTGTTGTTGACCTCACCTCACCCCACGCGAAAA GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGA CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTGCGGGCCCAGGACC GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCC IGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGC TICGETATICCCGTGCTCCAGAAGGCCGCCCATGGGCCACGTCCGCAAGGCCTTCAAGAGCC GCTCCTGCGTTTGGTGATTTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGAGTGCTGCANANGCTGTGCGANCGCGGCGCGAANAACGTGCTGGCCTTCGGCTTCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4029;
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Pred. No. 0.00e+00;
0; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "preliminary sequence for
human rRT cDNA insert of
plasmid pGRN121"
1342 C; 1255 G; 720 T; 25 OTHER.
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               015389-002930US
                                                                   APPLICATION NUMBER: US/08/854,050
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 10-APR-1997
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION UNDRER: 36,429
REFERENCE/DOCKET NUMBER: 0153
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
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Best Local Similarity 97.8%;
Matches 3702; Conservative
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OTHER INFORMATION:
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LOCATION: 1..4029
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                                                                        CACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCGGCCCACAGCCAGGCCG
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                                                         TCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCCAAGGGCGCCCG
                                                                                                                CCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGC
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APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Rakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Novel Telomerase
NUMBER OF SEQUENCES: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-854-050-173 STANDARD; DNA; UNC; 4029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
COUNTRY: United States of America
2IP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 173, Application US/08854050 Sequence 173, Application US/08854050 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCAGAT 3789
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STREET: TWC
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		Ę	CIGCIC	TGCT	GIGCIGGI	CIGCI	CIGC	AACG	GAACGGGC	GTGC	111	GTGG	GTGG		CGGGCAGG	AAGA	IIII AAGA	ນອນປອ	111111	CTIG	GCCTTG	ACTGC	II CAGCT(		) ປ	55555	1000	ACGCC				AGGAC		טאַטט	CAGG	
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	CACCAG	16666	111111	GCGNT		CAGCI	CAGCT	TGGGAT-	ີວ່	CCAGC	CCAGC	AGGCC	AGGCC	GCCCA	GCCA	AGACC	CCAGACCCGCCGAAGAAG	CCATO	CATC	TGGGA	TGGGA	GACAA	GACAA	500000	SCICE	CGCAG	CGCAG	CTTGG		SCIEC	GAGCTGCGG			CAGCC	CAGCC	,
			-0	SCTGC		rgtac	CGCCGCTGTACCAGCT	SCGTCT	SCGT	3C - TG	CCCCTGGGCCTGCCAGCCCCGGGTGC	CCAAG	CTGCCGTTGCCCAAGAGGCCCAGGCGTG	CCTGG	CCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACC	CTGCC		CCCAC	CTGGCACGCGCCACCCATCCG	3TCC-	GGCCACCACGTCCCTGGGACACC	CAGGC	GTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGG	00000	CTGAGGCCCAGCCTGACTGGCGCTCGG	TCCC	GACTCCCCGC	AGCTG	GITTCIGGAGCTGCTTGGGAACCACGCG	TGCGA	=6	ragag		PACAG	GCTCCGCCAGCACAGCACCCTGGCAGGT	
		AGCG	GAGCGGG	SGCAC	36CAC	သင္သင္လင္လ	110000	GAAN		CTGG	7CTG	STIGG	STTGC	BGGGT	1111	STCAC	STCACCTG	CACT	CACT	ACCAC	ACCAC.	TCCT	- ESSET	A D II D	CTGA	AGG-A	AGGGA	CTGG		CCCC	CAAGACGCACTGCCCGCT	TCTG	TOTICE	CAG	CCAG	
		999	=8	TGCT	HGCI	ညည	111111	GACC	GACC	TCCC		TGCC		GGCAC	- I I I	TGGT	GGACCGAGTGACCGTGGTTTCTGTGTGTGT	00000	- D	70000	10000	TCTA(	TCTAC	ט אַכּיַל.	CCAG	TGCC	CIGGGIICCAGGCCCIGGAIGCCAGG	TELL	1151	ACTG	ACTG	AGGG	CAGGGCTC	CTCC	1100	
	3=5	ACTG	GACGCACTGCG	TCACC	TCACCTO	- 52		TANT	TAGTO	09990		AAGTO	AAGTO	CGTTC	CGTT	CTGTG	CTGTC	TGGCA	1666	ATCGC	CACGCGGCCCCCCATCCACATCGC	CTTCC	CITIO	CAGGG	GAGGC	TTGG	CTGG	0000		GACGC	GACGC	2222		AGCTC	GIGCAGCIG	•
- 1		SACGO	BACGC	. ნ∶	5	CANGT	CCAGGTG	CACGC	CACGC	BAGGC	SAGGC	AGCCG	GCGGGGCAGTGCCAGCCGAAGT	ACGCC	ACGCC	GGTTT	GGTTT	- 5	GCTCTC	rccac	rccac	AAGCA	AAGCA	TATCT	ICTCT	AGGCC	AGGCC	ATGCG	ATGCG	CTCAA	CTCAA	SAGAA	CTGTGCCGGGAGAAGCCC	GGTGC	36760	;
		GACC	SACC	ACGTG	ACGTG	CTAC	CTAC	GCCA	- ACC 9	rcAGG	CAGG	STGCC	11600	AGCGG	1111	ACCGT	NCCGT	TGCG	511000	CCCA	CCCA	AGACC	I I I I	AATA	CAGC	TTCC	IIII STICC	SCAA	CAA	GTIC	CICCIC	9500	1 200	GCCT	GCCTGC	,
		ACGG	AACACGGT	GACG!	SGCGACGACGTGCTG	TGCG	AGCTGCGCCTAC	S		AGCG	CATAGCGTC	GGCAC	GGCAC	79900	75555	AGTG!	AGTG2	GAGG		2000	111	79009	19009	TACT	CTTCCTACTCAGCTCTC	TCTG	CIGGO	TACT	TACT	5555	11111	TGTG	1010	CCGTC	CACAGACCCCCGGTCG	<u>'</u>
	TGGAC	8	=8	ι,	GTGGG	6	CCCAGG	- 8	0555555	ACCAI	ACCAT	99929	00000	CTGAG	CTGAG	GACCG	GACCE	CTTIC	CITIO	ACGCG	ACGCG	TGTAC			<u> </u>	NTCTI		AGCGN	AGCGC	CCTAC	CCTAC	GTGTC	GGTGTC	GACCC	SACCO	
		CIG	CCTGC	ပ္ပ	50900	GGNTC	GGCTC	TCAGG	TCAGG	CTGGA	CTGGAACC	GAGGC	GAGGCG	recco	16000	- 5	11 11 GCGTG	CACCT	CACCTO	GCACC	- S	ອອວວວ	1111		GCCCT	AGACA	GACCA	22225	00000	STGCC	GTGCC	×	=8	ACACA	CACA	
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qq	1435	
Οy	L)	CGGCTTCGTGCGGGCCTGCCTGCGCGGCTGGTGCCCCCAGGCCTCTGGGGGCTCCAGGC 151
qa	1495	CATCTCCCTGGGGAAGCATGCCA 15
Qy	1512	CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCA 15
đ	ĽΩ	AGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCA 1614
Qy	1572	SCICICGCICCAGGAGCIGAAGGIGAAGAIGAGCGICCGGGACIGCGCIIGGCIGCGCA 1
qq	1615	CCTGG 16
Qy	1632	GAGCCCAGGGTTGGCTGTTCCGGCCGCAGAGCACCGTCTGCTGTGTGTTTTTTTT
qq	1675	CTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT
ΟŸ	1692	CAAGTICCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTTTT 175
ති	1735	TTCTACCGGAAGAGTGTCTGGA 17
Οy	1752	TGTCACGGAGACCACGTTTCAAAGAACAGCCTCTTTTTTTT
අු	1795	GCAAGTIGCAAAGCAITGGAATCAGACAGCACTTGAAGAGGGGGGGGGG
Qγ	1812	CAAGTIGCAAAGCATIGGAATCAGACAGCACTIGAAGAGGGTGCAGCIGCGGGAGCIGI 18
qa	1855	SACGICCAGACICC 19
Qγ	1872	GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCC
qq	1915	CTGACGGCTGCGGCCGATTGTGAACATGGACTACGTGGGGG 1
Qy	1932	CITCATCCCCAAGCCTGACGGCTGCGCCGAITGTGAACAIGGACIACGTGGGGG 19
QQ	1975	CCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGT 20
QY		CAGAACGTICCGCAGAGAAAAGAGGGCCGAGCGTCTCTCTCGAGGGTGAAGGCACTGT 2
QQ	2035	CAGCGTGCTCAACTACGAGCGGGCGCGCCCCGGGCTCCTGGGCGCCTCTGTGCTGG 2
Qy	2052	CGTGCTCAACTACGAGCGGGGGGGGCGCCCCCGGCCTCTTGTGCTGG 2
đ	2095	CCTGGACGAIATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGCGGGCC
δλ	2112	CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACC 2
QQ	2155	CCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGGGCGCTACGACACCATCCCCC 2
δλ	2172	GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGCTACGACACCATCCCCC 2
qq	2215	ACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGC 2
QY	2232	GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCCAGAACACGTACTGCGTGC 2
QQ	2275	TCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGCCACGTCCGCAAGGCCTTCAAGAGCC 2
οy	6	GICCAGAAGGCCGCCCAIGGGCACGCCCCAAGGCCCTTCAAGAGCC 2
QQ	2335	CGTCTCTACCTTGACAGCCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGG 2
Qy		STTCGTGGCTCACCTGCAGG 2
qq	2395	AGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGCTCCTCCCTGAATGAGGCCA 2
οy	$\exists$	GCCCGCTGAGGGATGCCGTCGTCGAGCAGAGCTCCTCCTCGAATGAGGCCA 2
QQ	2455	RGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGG 2
Qy	2472	CAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGG 2
qq	2515	GCAAGTCCTACGTCCAGGGGATCCCGCAGGGCTCCATCCTCCACGCTGCTCT 2574

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3612 GCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGC 3671
                                                                                  3732 AGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATC 3791
                                    3672 TGAGTGTCCAGCACCACCACCTCCCTACACCTCCCCACAGGCTGGCGCTCGGCTCCACCCC
                                                                      AGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATC
                        TGAGTGTCCAGCACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REALBLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CAURENT APPLICATION DATA:
APPLICATION NATE: 05-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                      : Two Embarcadero Center, 8th Floor
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
RECISTRATION NUMBER: 36,429
REFERENCE/DOORET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                      BP.
                                                                                                                                                                                                                    APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
CC APPLICANT: Chapman, Karen B.
CC APPLICANT: Marin, Gregg B.
APPLICANT: Marin, Gregg B.
APPLICANT: Marin, Gregg B.
TITLE OF INVENTION: Novel Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Emhr.
CITY: Sar
                                                                                                                                                                                   US-08-851-843-173 STANDARD; DNA; UNC; 4029
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FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNDBER:
TILING DATE: 01-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION 536
PRIOR APPLICATION TO S36
PRIOR APPLICATION NUMBER: US 08/844,419
FILING DATE: 18 APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America 2IP: 94111
                                                                                                                                                                                                      Sequence 173, Application US/08851843 GENERAL INFORMATION:
APPLICANT: Cech. m.-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                    Score 3468; DB 21;
Pred. No. 0.00e+00;
0; Mismatches 78;
                   /note= "preliminary seg
human TRI CDNA insert o
plasmid pGRN121"
1342 C; 1255 G; 720 T;
                                                    Query Match 91.3%;
Best Local Similarity 97.8%;
Matches 3702; Conservative
            LOCATION: 1..4029
OTHER INFORMATION:
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                                      SEQUENCE 4029 BP; 687 A;
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Sequence 4, Application US/08912951
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Linguer, Joachim
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Taren B.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBITILE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "nucleic acid sequence with an open reading frame encoding a delta-182 variant polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3855;
                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: POLYPEPTIGE"
SEQUENCE 3855 BP; 651 A; 1300 C; 1226 G; 678 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product- "delta-182 variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 3391; DB 22;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                 PRICR APPLICATION: 433
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
CLASSIFTCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                           IELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3855 base pairs
                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 89.3%;
Best Local Similarity 95.2%;
Matches 3603; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: 1.3855
LOCATION: 1.3855
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                          CLASSIFICATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
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Qy       2353       CGTCTCTACCTTGACAGACCTCCAGCC         Db       2344	ന വ ന	Db 2399 CAGCCTGTGCTACGGCGACATGGAGAA [	2519	Db 2579 GACAGTGGTGAACTTCCTGTAGAACA	Qy 2833 GCGGCCCACGCCTATTCCCTGGTG Db 2699 GCAGAGCGACTACTCCAGCTATGCCCC QY 2893 GCAGAGCGACTACTCCAGCTATGCCCC	Db 2759 CGCTTCAAGGCTGGGAGGAACATGCC 	3013	3073 (2939.)	3133	3193 CIGCIAC 3193 CIGCIAC 3059 CGGCCCT	3253	3313	3373	Db 3239 ATGCCTCAGACTTCAAGACCATCCI 
1273 1321 1333 1381		1501 CAACGAACGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAACCATGCCAA 156	1573 1621 1633	1681 CAAGTTCCTGCACT	1753 TGTCACGGAGACCACGTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTCTGGGGG 1801 CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGGGTGCAGCTGCGGGAGCTGTC 1801 CAAGTTGCAAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTC 1813 CAAGTTGCAAAAGCAATCAGAACAGCAGCTGCAGGGGGGCTGTC 1813 CAAGTTGCAAAAGCAATCAGAACAGCAGCTGCAGGGGGAGCTGTC	1861 GGAAGCAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCTGCTGACGTCCAGACTCCG 192	<ul> <li>1921 CITCATCCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 1980</li> <li>1933 CITCATCCCCAAGCCTGAGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 1992</li> </ul>	o 1981 CAGAACGTTCCGCAGAGAAAAGAGCGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT 2040 	<ul> <li>2041 CAGCGTGCTCAACTACGAGCGGGCGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGG 2100</li> <li>111111111111111111111111111111111111</li></ul>	2 2101 CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGCG	2161 GCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGTACGACATCCCCCA 2220 	o 2221 GGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG	b 2281 TCGGTATGCCGTGGTCCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCC 2340 	5 2341 CGTC 2344
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3252 3118 3178 2458 2518 2712 STCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAA 2578 2832 2758 2952 2818 TIGAACAGCCTCCACACGGTGTGCACCAACATCTA 2878 2938 2998 3192 3058 3312 3238 2344 2532 2398 2592 2652 2638 GCGGCCTGCTGCTGGATACCCGGACCCTGGAGGT 2698 3012 3132 CTGGACTGATGGCCACCGCCCACAGCCAGGCCGA 3492 CGTACATGCGACAGTTCGTGGCTCACCTGCAGGA 2412 STCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG 2472 ATCCGGAGGGCTCCATCTCTCACGCTGCTCTG TIGTTGGTGACACCTCACCTCACCCACGCGAAAAC AGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCA ITTTCCTGCGCGTCATCTCTGACACGGCCTCCCT AGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT TEGACTGATGGCCACCCGCCCACAGCCAGGCCGA ACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT GGACCTCCATCAGAGCCAGTCTCACCTTCAACCG CACTCCTGGGGTCACTCAGGACAGCCCAGACGCA ACCTGACTGCCCTGGAGGCCGCAGCCAACCCGGC GCTTCATGTGCCACCACGCCGTGCGCATCAGGGG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3855;
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 56..2476
LOCATION: 56..2476
OTHER INFORMATION: /product= "hTRI"
OTHER INFORMATION: /note= "clone #712562"
SEQUENCE 3855 BP; 651 A; 1300 C; 1226 G; 678 T; 0 OTHER.
                                                                                                                   NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002500US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 3855 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 3391; DB 22;
Pred. No. 0.00e+00;
0; Mismatches 1;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.2%;
Matches 3603; Conservative
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                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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                                   GAGIGICCAGCACACCIGCCGICTICACTICCCCACAGGCIGGCGCICGGCICCACCCCA 3538
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                                                                                                                                                                                                                                                                                                        3733 GGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3792
                                                                                                                                                                        CACACCCAGGCCCGCACCGCTGGGGAGTCTGAGGCCTGAGTGTGTTTGGCCGAGGCCTG
                                                                                                                                                       CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT
                 APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morih, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
APPLICANT: Telomerase Reverse Transcriptase
NUMBER OF INVENTION: Telomerase Reverse Transcriptase
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY. CALL STATE COUNTRY. COUNTRY. COUNTRY. USA ZIP: 94111-3834
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFFWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/911,312 FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                          .T 10
US-08-911-312-18 STANDARD; DNA; UNC; 3855
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FILING DATE: 25-APR-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-CCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/08911312
Sequence 18, Application US/08911312
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
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qq	1741	GTCACGGAGACCACGTTTCAAAAGAACACGCTCTTTTCTACCGGAAGAGTGTCTGGAG 180
QY	1753	
qq	1801	AAGTIGCAAAGCATIGGAATCAGACAGCACTIGAAGAGGGGTGCAGCTGCGGGGGGGTC 186
οy	1813	TICCAAAGCATIGGGAAICAGAGCACTIGAAGAGGGGGGGGGG
đ	1861	~
ΟY	1873	GAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCC
qq	1921	SCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 1
Qy	1933	CATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC 19
Dp	1981	AGAACGTTCCGCAGAGAAAAGAGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT 204
Qγ	1993	AACGITCCGCAGAGAAAAGAGGGCCGAGCGICICICICICICICIC
QQ	2041	ACTACGAGCGGGCGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGG 210
QY	2053	CTGCTCAACTACGAGCGGGGCGCGCCCCGGCTCCTGGGCGCCTCTGTGTGTTTTTT
DP	2101	GACGATATCCACAGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACC
QY	2113	THE STATE OF THE S
QQ	2161	TTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA 222
Qy	2173	CCGCCTGAGCTGTACTTTGTCAGGTGGGTGTGACGGCGCGCTACGACGACCATCCCCCA 223
QQ	2221	TCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCG
δy	2233	GACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTACGTGGGGGGG 229
qq	2281	CCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA 234
Qy	2293	CGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCA 235
qq	2341	GTC
QY	2353	GTACATGCGACAGTTCGTGGCTCACCTGCAGGA 241
qq	2344	23
δy	2413	ACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG 24
qq	2344	
Οy	2473	TCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCC
qq	2345	STCCAGTGCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTCTG
Qy	2533	
q	2399	AGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT 245
Qy	2593	CCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT 265
QQ	2459	TTGGTGACACC
Qγ	2653	CTCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCCACGCGAAAAC 27
qq	2519	TICCICAGGACCCIGGICCGAGGIGICCCIGAGIAIGGCIGCGIGGIGAACTIGCGGAA 257
QY	2713	TCCTCAGGACCCTGGTCCCAGGTGTCCTGGTATGGCTGCGTGGACTTGCGGAA 2
q	2579	AGAAAGACGAGGCCTGGGTGGCACGCTTTTGTTCAGAT 263
Οy	2773	3TGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTC

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CCCGCGATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTAC
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Sequence 13, Application US/08951733
Sequence 13, Application US/08951733
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: NOVEL GENES ENCODING TELOMERASE PROTEINS
NUMBER OF SEQUENCES:
ADDRESSEE: Amgen Inc.
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                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

IP: 91320-1789

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,733
FLING DATE: 16-OCT-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2848; DB 22;
Pred. No. 0.00e+00;
0; Mismatches 0;
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APPLICATION NUMBER: US 08/873,039
FILING DATE: 11-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,189
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: A-433B TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                         ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (805) 499-8011
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (805) 447-6504
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SEQUENCE 2848 BP; 437 A; 978
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Best Local Similarity 100.0%;
Matches 2848; Conservative
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2639 GCCGGCCCACGACTACCCCTGGTGCGCCCTGCTGCTGGATACCCGGACCCTGGAGGT
                                                       2833 GCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGT
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TCACCA IIIII	GGGCGI			TGTACC	ILLI	SGCGTC	SGCGTCTG	SCCIGO			CCTGGG	CCTGGG	CTGCC	TIGCCA	CCCACC	CCCACC	STCCCI	STCCCI	CAGGCG			CTCCCC	CTCCCC	AGCTGC	AGCTGC	TGCGAG	TGCGAG	3666		ACAGCA	ACAGCA	CAGGCC
GGCCT	GAGCG	GAGCG	GGCACGCTGCGCGCTC	25225	1111	CCGAA	CCGAA	CCTGG			GGGGT	- - -	GTCAC	GTCAC	CCACT	CCACT	ACCAC	ACCAC		10000		AGGGA	CCAGGGACTCCCCGCAGG	TCTGG	TCTGG	ວອວວວ	1111	CTCTG	GGCTCTGTG	CCGCCAGCACAGCAGCCCC	CCAGC	೨೦೦೦೨,
	ອອອອວອ			000000	000000	TGGACC	TGGACC	GGTCCC			TGGGCA	TGGGCA	TGTGGI	TGTGGT	CACGCG	CACGCG	000000	ဝင္ခုဇင္ခင္	GTGTAGGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAA(    -  -  -  -  -  -  -  -  -  -  -  -		CCTCCTTCCTACTCCACTCTCTCTCTCTCTCTCTCTCTC	GATGCC	CCTGGATGC	CCTGTI	CCTGT1	GCACTG	GCACTG	CCAGGG	CCAGGG	SCICCO	SCICCO	GTGTACGGCTTCGTGCGGGCCTGCCTGCGGCTGGTGCCCCCAGGC
000000	GCACT	GCACT	GTTCA	GTGTG	GTGTG	GCTAG	GCTAG	99008		CGAAG	CCCGT	HILL	TTCIG	TTCTG	TCTGG	11111 TCTGG	ACATO	ACATO	CACTI		CTGAG	CCCTG	1111	ວວອອວເ	200000	AAGAC	AAGAC	SAAGCC	NAGCC	SCAGCT	CAGCT	ອວວອວເ
000000	ACCGAC	ACCGAC	GTGCTG	TACCAG	TACCAG	CCACAC	CCACAC	AGGGAG			CGGACG	CGGACG	CGTGGI	CGTGG	GCGCTC	GCGCTC	CCATCC	CCATCC	ACCAAC	10000	AGC1-C	TCCAGG	GTTCCAGGCC	CAAATO	CAAATO	CICCIC	CTCCTC	CGGGAG	CGGGAC	CTGGTC	стестс	TGCCTG
1	CGGTG	 	ACGACO	GCGCCI	1111	90000	00000	GCGTC			CGGAG	CGGAG	GTGAC	GTGAC	AGGGT	AGGGT	000000	00000	CCGAG		TACTO	TGGGT	TGGGT	ACTGG	ACTGG	GGGTG	GGGTG	GTGCC	GTGCC	GTCGC	GICCC	22999
GGACG 	CAACA	CAACA	11111	CAGCT	CAGCT	ວຍຍວວ	09900	CCATA	WI WIN		TGAGC	TGAGC	ACCGA	IIIII	TTTGG	TTTGG	99292	NCGCGG	GTACG			CTTTC	CTTTC	GCGCT	GCGCT	CTACG	CTACG	TGTCT	FILLI		CCCCC	CGTGC
GCTGCJ	CCTGCC	CCTGC		BGCTCC	36CTC	TCAGG	TCAGG	CTGGA		SAGGC	TGCCCC	TGCCCC	SCGTGC	SCGTGC	CACCTC	CACCTC	GCACC	SCACC.		? ;		GACCAI	GACCAT	70000	20000	GTGCCC	GIGCC	AGCCGC	AGCCGC	CACAG	CACAG	CGGCT1
11CGO	AGCTA	AGCTA	CTGCG	CIGGI	CTGGT	GCCAC	GCCAC	00000		- CCAG	29299	1111	AGGAC	AGGAC	GAAGC	GAAGC	CGCCA	CGCCA		, ,		GTGGA	GTGGA	LOOSO	CGCCT	GCGCA	GCGCA	CCAGC	CCAGC	GAGGA	GAGGA	GTGTA
TTCGCCTTCGCGCTGCTGGACGGGCCCGCGGGGGCCCCCCCGAGGCCTTCACCACCACCACACACA	STGCGC	GIGCGC	CTGCTGCTGCGCCGCGGGGGACGACGTGCTGGTTCACCTGCT( 	TTGTG		EGCCCT		TOGGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGCCTGCC	##9791	CCGCGTGCCAAGAAGCGCGCGGGGGGATTCCCAAAGTCTGCCAAAGTCTCCAAAAGTCTCCCAAAAGTCTCCAAAAGTCTCCAAAAGTCTCCAAAAAGTCTCCAAAAAGTCTCCAAAAAGTCTCCAAAAAGTCTCAAAAAAGTCTCAAAAAAAA	AGGCGT		CCGGGC		GCCGAA	GCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCAC	GTGGGCCGCCAGCACGCGGGCCCCCCATCCACATCGCGGCCACCACCTCCTGGGAC	STGGGC	ACGCCTTC 1111111 ACGCCTTC		GAGCAGO	AGGCTC		TGCCC	THECCCGCCTGCCCCAGCGCTACTGGCCAATGCGGCCCCTGTTTCTGGAGCTGCTTG	PACCAC		STCACC		GAGGAGGAGGACACAGACCCCGTCGCCTGGTGCAGCTGCTG	SAGGAG	TGGCAG
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2176 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.2%;
Matches 1924; Conservative
                                                                                                                                                                            single
                                                                                                                                                                                                                           NAME/KEY: -
LOCATION: 1..2176
OTHER INFORMATION:
                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
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APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Manman, Karen B.
APPLICANT: Morin, Greag B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, Milliam H.
APPLICANT: ANDRESSE: 335
CORRESPONDENCE ADDRESS: 335
CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                      CGGGACGGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACC 2700
                        ACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGG 2640
                                    2642 CGGGACGGCTGCTCCTGCGTTTGGTGATTTTCTTGTTGGTGACACCTCACCTCACC 2701
                                                                                                                       CACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTG 2760
                                                                                                                                    2702 CACGCGAAAACCTICCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTG 2761
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COMPUTER: IBM PC Compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: U4-Aug-1997
CLASSIFICATION APA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAX-1997
CLASSIFICATION NUMBER: US 08/854,050
FILING DATE: 09-MAX-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAX-1997
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US-08-912-951-3 STANDARD; DNA; UNC; 2176
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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FILING DATE: 25-APR-1997
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Sequence 3, Application US/08912951
GENERAL INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2176;
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SEQUENCE 2176 BP; 432 A; 678 C; 642 G; 422 I; 2 OTHER.
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Pred. No. 0.00e+00;
0; Mismatches 3;
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0cT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
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CTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGG
                                                     and
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                                                                                                                                                                                                                                                                                                                        Sequence 36, Application US/09026981
Sequence 36, Application US/09026981
GENERAL INFORMATION:
APPLICANT: Counter, Christopher M.
APPLICANT: Meyerson, Matthew
APPLICANT: Weinberg, Robert A.
TITLE OF INVENTION: Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: WHI97-11p4AM
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US-09-026-981-36 STANDARD; DNA; UNC; 3346
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PRIOR APPLICATION DATA:
APPLICATION ATA:
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/064,322
FILING DATE: 30-0CT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,762
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FILING DATE: 20-MAY-1997
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CLASSIFICATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
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REGISTRATION NUMBER: 32,
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US
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STATE:
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E		SEQUENCE CHARACTERISTICS: LENGTH: 3346 base pairs	TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	SEQUENCE 3346 BP; 617 A; 102	Ouery Match 41.5%; Score 1575; DB 23; Length 3346; Best Local Similarity 85.2%; Pred. No. 0.00e+00; Matches 1975; Conservative 0. Mismatches 1; Indale 341; Cane 2.	971 GGGTTGGCTGTTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCC 1030			1701 IGCACIGGCTGAIGAGIGIGIACGICGICGAGCIGCTCAGGGTCITICITIIAIGTCACGG	> 1091 AGACCAGTTTCAAAAGAACAGGTCTTTTTCTACCGGAAGAGTGTCTGGAGGAAGTTGC 1150 	1151 AAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAG		1211 AGGTCAGGCAGCATCGGGAAGCCAGCCCGCCCTGCTGACGCCCAGACTCCAGACTCCGCTTCATCC	1881 AGGTCAGGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCC	2 1271 CCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGT 1330 11	1331 TCCCCACACACACCCCCCCCCCCCCCCCCCCCCCCCCC	2001 TCCGCAGAGAAAAGAGGCCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGC	1391	2061 TCAACTACGAGCGGGGGGGCGCCCCGGCCTCTGGGCGCCTCTGTGCTGGGCCTGGGACG 2120	1451 ATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGCGGGCCCAGGACCCGCCGCTG 1510	2121 ATATCCACAGGGCCTGGCGCACCTTCGTGCTGTGGGGGCCCCAGGACCCGCCGCTG	1511 AGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGTACGACCACCACCAGGACAGGC	1571	2241 TCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACGGTACCGTACCGTACCGTACCGTACGTA	1631 CCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTC	11111111111111111111111111111111111111	) 1686 1686	2361 CCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGCAGCC 2420	0 1686 1686	7 2421 CGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCGAATGAGGCCAGCAGCAGTGGCC 2480	) 1687
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PACGCTTCATGTGCCACCACGCGTGCGCATCAGGGGCAAGTCCT 2540 CCGCAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGG 2768 CCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCA 3GGCCAAGGCCCCCCCCTCTGCCCTCCGAGGCCGTGCAGT GGATCCCGCAGGCTCCATCTTCACGCTGCTGCAGCCTGT STGTCCCTGAGTATGGCTGCGTGAACTTGCGGAAGACAGTGG AGAACGCAGCCGAAGAAACATTTCTGTCGTGACTCCTGCGGTGC SGGAGCTGGGCCTGTGACTCCTCAGCCTCTGTTTCCCC CATTCCTGCTCAAGCTGACTCGACACCGTGTCACCTACGTGCCAC SGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGT AGAACAAGCIGITIGCGGGGATICGGCGGGGCGGGCTGCTCCTGC **ICTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCA** NCAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAG CAGAGATGGAGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTTC JATTCCTGCTCAAGCTGACTCGACACGTGTCACCTACGTGCCAC GACAGCCCAGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGC PGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCC AGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCC 

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        GGCTCTACGTCCCAGGGAGGGGGGGGGCCCACACCCAGGCCCGCACCGCTGGGAGTCT
                                                                                                                              TGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACCACCTGCCGTCTTCACT
                                                                                                                                                  3642 TGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACT
                                                         3522 GGCTCTACGTCCCAGGGAGGAGGGCGGCCCACACCCAGGCCCGCACCCCCGCGGGAGTCT
                                                                                                                                                                     3009 TCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGG
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cech, Thomas R.
APPLICANT: Cach, Thomas R.
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Novel Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Corew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843 FILING DATE: US-MAY-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                        STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                              3069 CTTCCACTCCCCACATAGGAATAGTCCATCCCCAGAT 3105
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US-08-851-843-100 STANDARD; DNA; UNC; 2171
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APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
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FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
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APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America 2IP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       Sequence 100, Application US/08851843
Sequence 100, Application US/08851843
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 40.0%; Score 1520; DB 21; Length 2171; Best Local Similarity 90.8%; Pred. No. 0.00e+00; Matches 1915; Conservative 1; Mismatches 5; Indels 188;
                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 22..1716
OTHER INFORMATION: /note= "ECORI-NOt1 insert of
OTHER INFORMATION: clone 712562 encoding 63 kDa
OTHER INFORMATION: telomerase protein"
                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: telomerase protein" SEQUENCE 2171 BP; 433 A; 667 C; 641 G; 429 T; 1 OTHER.
      015389-002930US
REFERENCE/DOCKET NUMBER: 01538
TELECHONICATION INFORMATION: ..
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 2171 base pairs
TYRE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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δŏ	2471 AGCAGTGGCC	AGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCGCGCGCG	S 2	,
QQ			a ò	1/38 CIGCATGICCG 1111111111111111111111111111111111
δλ	2531 GGCAAGTCC	TACGTCCAGTGCCAGGGATCCCGCAGGGGTCCATCCTCCCACGCTGCTC 2590	7 A	1796 GCTGAGTGTCC
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ογ	2651 CIGCICCIG	CTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCCACGCGAAA 2710	Š 2	3/30 CCAGGGCCAGG
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do yo	958 ATGCCGGCCC 	ATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGGTACCCGGACCCTGGAG 1017 	5800	Sequence 100, Apsendence 100,
qq	1018 GIGCAGAGCC	107	888	APPLICANT: C
Qy	2891 GTGCAGAGC		មួម	APPLICANT: N
qq	1078 CGCGGCTTCA	GGGGCTTCAAGGCTGGGAAGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGGCTGAAG 1137	ខមុខ	APPLICANT: N APPLICANT: E
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da do	1138 TGTCACAGCC   1138 TGTCACAGCC	IGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATC	8888	CORRESPONDENC ADDRESSEE: STREET: Tw
QQ	1198 TACAAGATCC	CICCIGCIGCAGGGIACAGGIIICACGCAIGIGGCGCAGCICCCAIII 1257	ខូខូ	CITY: San STATE: Cal
ογ	3071 TACAAGATCC		ខ្លួន	COUNTRY: CZIP: 94111
අ ද		CATCAGCAAGTTTGGAAGACCC-ACATTTTCCTGCGCGTCATCTCTGACACGC-TCC 1315	388	COMPUTER REAL MEDIUM TYPE COMPUTER:
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a &	1316 CTCTGCTACT 	CTCTCCTAACTCCATCCTGAAACCAAGAACGAGGATGTCGCTGGGGGCCAAGGGCGCC 1375 	888	CURRENT APPLI APPLICATION FILING DATE
g :	1376 GCCGGCCCTC		888	CLASSIFICAT PRIOR APPLICA APPLICATION
3 8		CINCCLICCERGENCEIGENERGIGGETIGIGCCACCARGCATICCIGGICARG 3310	888	FILING DATE CLASSIFICAT
3 8		v .	388	PKIOK APPLICA APPLICATION FILING DATE
q o	1496 CAGCTGAGTC 	CAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCGGAGCCAACCCG 1555	3888	CLASSIFICAT PRIOR APPLICA APPLICATION FILING DATE
Q	1556 GCACTGCCCT	16	ខម	CLASSIFICAT PRIOR APPLICA
οy	3431 GCACTGCCCT		888	APPLICATION FILING DATE
අ	1616 GAGAGCAGAC 	GAGAGCAGACCAGCACCCTGTCACGCCGGGTTATACGTCCCAGGAGGGGGG 1675	3888	CLASSIFICAT ATTORNEY/AGEN NAME: Appl
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                                           AGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCCACCACGCGTGCGCATCAGG
                                                                                                        TGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGGATTCGGCGGGACGGG
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                                                                                                                                                                                                                         5; Indels 188;
                                                                                                                                                                                                    Length 2171;
                                                                                                                                               /note= "EcoRI-NotI insert of
clone 712562 encoding 63 kba
telomerase protein"
667 C; 641 G; 429 T; 1 OTHER.
                                                                                                                                                                                                   Score 1520; DB 21;
Pred. No. 0.00e+00;
1; Mismatches 5;
  015389-002930US
REFERENCE/DOCKET NUMBER: 0153
TELECOMONICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISICS:
LENGTH: 2171 base pairs
                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                              SEQUENCE 2171 BP; 433 A; 667
                                                                                                                                                                                                  Query Match
Best Local Similarity 90.8%;
Matches 1915; Conservative
                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                          NAME/KEY: CDS
LOCATION: 22..1716
OTHER INFORMATION: /
OTHER INFORMATION: ¢
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Search completed: Fri Dec 25 08:54:06 1998 Job time: 8861 secs.